

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

6149410

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>Barak</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>308-4427</u>	AA Sequence (#) <u>4</u>	Dialog _____
Searcher Location: <u>CM1-1E17</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>3/22/01</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>3/23/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <u>aps504</u>
Technical Prep Time: <u>4</u>	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:52:01 : Search time 171.82 seconds

10,914 Million cell updates/sec

Title: US-09-147-362-10

Perfect score: 1 LUNSMCKGRWCVYIS 16

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:
2: SP-bacteria:
3: SP-fungi:
4: SP-human:
5: SP-invertebrate:
6: SP-mammal:
7: SP-mbc:
8: SP-organelle:
9: SP-phage:
10: SP-plant:
11: SP-protist:
12: SP-virus:
13: SP-vertebrate:
14: SP-unclassified:
SPREMBL_15:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	216	12	091EB6 human immun
2	93	100.0	216	12	091EB6 human immun
3	91	97.8	219	12	091EB6 human immun
4	90	96.8	130	12	091EB6 human immun
5	89	95.7	242	12	091EB3 human immun
6	87	93.5	116	12	040451 human immun
7	87	93.5	118	12	040451 human immun
8	87	93.5	120	12	091H02 human immun
9	87	93.5	131	12	09WR05 human immun
10	87	93.5	131	12	091H02 human immun
11	87	93.5	137	12	091H02 human immun
12	87	93.5	146	12	09WR05 human immun
13	87	93.5	213	12	091EB3 human immun
14	87	93.5	214	12	091EB6 human immun
15	87	93.5	216	12	091EB6 human immun
16	87	93.5	342	12	011942 human immun
17	87	93.5	532	12	091EB3 human immun
18	87	93.5	532	12	091EB3 human immun
19	87	93.5	548	12	091EB6 human immun

20	87	93.5	871	12	057073 human immun
21	87	93.5	871	12	057074 human immun
22	87	93.5	872	12	057072 human immun
23	87	93.5	900	12	090N88 human immun
24	87	93.5	114	12	040448 human immun
25	86	92.5	116	12	040458 human immun
26	86	92.5	116	12	040458 human immun
27	86	92.5	116	12	011941 human immun
28	86	92.5	117	12	090EF2 human immun
29	86	92.5	124	12	091H07 human immun
30	86	92.5	132	12	091H04 human immun
31	86	92.5	134	12	091H04 human immun
32	86	92.5	162	12	091EB3 human immun
33	86	92.5	200	12	091EB3 human immun
34	86	92.5	200	12	091EB3 human immun
35	86	92.5	210	12	091EB7 human immun
36	86	92.5	213	12	091EB4 human immun
37	86	92.5	220	12	091EB9 human immun
38	86	92.5	225	12	091EB0 human immun
39	86	92.5	234	12	091EB2 human immun
40	86	92.5	234	12	091EB2 human immun
41	86	92.5	517	12	091EB2 human immun
42	86	92.5	532	12	091EB0 human immun
43	86	92.5	545	12	091EB7 human immun
44	86	92.5	547	12	091EB6 human immun
45	86	92.5	879	12	09W109 human immun

ALIGNMENTS

RESULT 1
ID 091EB5 PRELIMINARY: PRT: 216 AA.
AC 091EB5:
DT 01-OCT-2000 (TREMBL) 15, Created
DT 01-OCT-2000 (TREMBL) 15, Last sequence update
DT 01-OCT-2000 (TREMBL) 15, Last annotation update
DE CP41 (FRAGMENT).
GN ENV.
OS Human Immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676.
RA SOURCE FROM N.A.
RA STRAIN=ECF07
RA Roques P., Robertson D., Sandline S., Christel D., Francois S.,
Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.
BL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ236594; CAB96243.1;
FT NON_CODING
FT 1
FT 216
SQ SOURCE 216 AA: 25027 MW: 413AB9BB1B4FC9A CRC64:

Query Match 100.0%: Score 93: DB 12: Length 216:
Best Local Similarity 100.0%: Pred. No. 1e-07:
Matches 16: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
Oy 1 LUNSMCKGRWCVYIS 16
Db 47 LUNSMCKGRWCVYIS 62

RESULT 2
ID 091EB6 PRELIMINARY: PRT: 219 AA.
AC 091EB6:
DT 01-OCT-2000 (TREMBL) 15, Created
DT 01-OCT-2000 (TREMBL) 15, Last sequence update
DT 01-OCT-2000 (TREMBL) 15, Last annotation update
DE CP41 (FRAGMENT).

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GN ENV.
RC Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCF14;
RA Philippe M.;
RA Roques P.; Robertson D.; Sandrine S.; Christel D.; Francois S.;
RA Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL: U230404; CAB96242.1; -.
FT NON-TER
FT 219
SO SEQUENCE 219 AA; 25353 MW; F65829EB01520D91 CRC64;

Query Match 100.0%; Score 93; DB 12; Length 219;
Best Local Similarity 100.0%; Pred. No. 1,1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LNSMCKGRKLYCYTS 16
DB 57 LNSMCKGRKLYCYTS 72

RESULT 3
091EC8 PRELIMINARY; PRT; 219 AA.
ID 091EC8
AC 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCF02;
RA Roques P.; Robertson D.; Sandrine S.; Christel D.; Francois S.;
RA Philippe M.;
RA *Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.*;
RA Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL: AJ236591; CAB96240.1; -.
FT NON-TER
FT 219
SO SEQUENCE 219 AA; 25363 MW; 85C2DC5B5528907 CRC64;

Query Match 97.8%; Score 91; DB 12; Length 219;
Best Local Similarity 93.8%; Pred. No. 2,2e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 LNSMCKGRKLYCYTS 16
DB 56 LNSMCKGRKLYCYTS 71

RESULT 4
091H09 PRELIMINARY; PRT; 130 AA.
ID 091H09
AC 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NC NCBI_TaxID=11676;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-97CM798;
RA Yang C.; Gao F.; Fonjuno P.N.; Zekeng L.; van der Groen G.;
RA Plaszek D.; Schable C.; Lal R.B.;
RT *Phylogenetic analysis of protease and transmembrane regions of HIV
RT Type 1 group O.*;
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL: AF229235; AAF71912.1; -.
FT NON-TER
FT 130
SO SEQUENCE 130 AA; 15993 MW; 5385769A336344EA CRC64;

Query Match 96.8%; Score 90; DB 12; Length 130;
Best Local Similarity 93.8%; Pred. No. 2e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 LNSMCKGRKLYCYTS 16
DB 40 LNSMCKGRKLYCYTS 55

RESULT 5
091E31 PRELIMINARY; PRT; 242 AA.
ID 091E31
AC 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE TM, GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCF112;
RA Roques P.; Robertson D.; Souquiere S.; Diamond F.; Mauchere P.;
RA Deplenne C.; Brun-Vezinet F.; Dormont D.; Simon F.O.;
RT *Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates.*;
RT Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL: AJ243366; CAB96336.1; -.
FT NON-TER
FT 242
SO SEQUENCE 242 AA; 27539 MW; DEBA73DF0E8A6FD7 CRC64;

Query Match 95.7%; Score 89; DB 12; Length 242;
Best Local Similarity 87.5%; Pred. No. 5,2e-07;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 LNSMCKGRKLYCYTS 16
DB 64 LNSMCKGRKLYCYTS 79

RESULT 6
040459 PRELIMINARY; PRT; 116 AA.
ID 040459
AC 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JAN-2000 (TREMblrel. 13, Last annotation update)
DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCF09 O.
RA Ribollet-Ruche F.; Ekasa E.; Peeters M.; Delaporte E.;
RA Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
RL EMBL: Y09775; CAA70914.1; -.

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DR INTERPRO: IPR000328; .
DR PFAM: PF00517; GP41; 1.
DR TRANSMEMBRANE: 1
FT NON_TER 116 116
SO SEQUENCE 116 AA; 13975 MW; 1283000DDA1A032 CRC64;

Query Match 93.5%; Score 87; DB 12; Length 116;
Best Local Similarity 93.8%; Pred. No. 5.7e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 1 LINSMCKGRVLYCYTS 16
DB 39 LINSMCKGRVLYCYTS 54

RESULT 7
Q040451 PRELIMINARY; PRT: 118 AA.
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GROUP O;
RA Bilbolet-Ruche F., Ekasa E., Peeters M., Delaporte F.;
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: Y09779; CAAY018.1; .
DR INTERPRO: IPR000328; .
DR EMBL: AF131577; AAD42745.1; .
DR TRANSMEMBRANE: 1;
KW Transmembrane.
FT NON_TER 118 118
FT NON_TER 1
SO SEQUENCE 118 AA; 14094 MW; C4491740918DE154 CRC64;

Query Match 93.5%; Score 87; DB 12; Length 118;
Best Local Similarity 93.8%; Pred. No. 5.7e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 1 LINSMCKGRVLYCYTS 16
DB 39 LINSMCKGRVLYCYTS 54

RESULT 8
Q09IHU2 PRELIMINARY; PRT: 120 AA.
ID Q9IHU2
AC Q9IHU2
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97ES205;
RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lal R.B.;
RT Phylogenetic analysis of protease and transmembrane regions of HIV
FT AIDS Res Hum Retroviruses 16:1075-1081(2000).
DR EMBL: AF229242; AAF71919.1; .
FT NON_TER 1 1

FT NON_TER 120 120
SO SEQUENCE 120 AA; 14322 MW; 510030863AC87929 CRC64;

Query Match 93.5%; Score 87; DB 12; Length 120;
Best Local Similarity 93.8%; Pred. No. 5.7e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 1 LINSMCKGRVLYCYTS 16
DB 33 LINSMCKGRVLYCYTS 48

RESULT 9
Q9WR05 PRELIMINARY; PRT: 131 AA.
ID Q9WR05
AC Q9WR05
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=32702;
RA Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype differentiation."
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF131577; AAD42745.1; .
DR INTERPRO: IPR000328; .
DR EMBL: AF00517; GP41; 1.
DR TRANSMEMBRANE: 1;
KW Envelope Protein.
FT NON_TER 131 131
FT NON_TER 1
SO SEQUENCE 131 AA; 15736 MW; 1053P8543F8B698 CRC64;

Query Match 93.5%; Score 87; DB 12; Length 131;
Best Local Similarity 93.8%; Pred. No. 6.2e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 1 LINSMCKGRVLYCYTS 16
DB 40 LINSMCKGRVLYCYTS 55

RESULT 10
Q9IHUO PRELIMINARY; PRT: 131 AA.
ID Q9IHUO
AC Q9IHUO
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97ES202;
RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lal R.B.;
RT Phylogenetic analysis of protease and transmembrane regions of HIV
FT AIDS Res Hum Retroviruses 16:1075-1081(2000).
DR EMBL: AF229244; AAF71921.1; .
FT NON_TER 131 131

SO SEQUENCE 131 AA: 15736 MW: 1053F65345FE698 CRC64:

Query Match 93.5% Score 87: DB 12: Length 131:
Best Local Similarity 93.8% Pred. No. 6.2e-07:
Matches 15: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 1 LNSMCKGRVLCYTS 16
DB 40 LNSMCKGRVLCYTS 55

RESULT 11

ID 091HVS PRELIMINARY: PRT: 137 AA.

AC 091HVS
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).

GP41.

Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

RP SEQUENCE FROM N.A.

RC STRAIN=97CM751;

RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,
Pleniazek D., Schable C., Lal R.B.,

*Phylogenetic analysis of protease and transmembrane regions of HIV

RT AIDS Res Hum. Retroviruses 16:1075-1081(2000).

DR EMBL: AF229229; AAF71906.1; "

FT NON_TER 1

FT NON_TER 137

SO SEQUENCE 137 AA: 16494 MW: 55C470860816893 CRC64:

Query Match 93.5% Score 87: DB 12: Length 137:
Best Local Similarity 93.8% Pred. No. 6.5e-07:
Matches 15: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 1 LNSMCKGRVLCYTS 16
DB 40 LNSMCKGRVLCYTS 55

RESULT 12

ID 09WRV2 PRELIMINARY: PRT: 146 AA.

AC 09WRV2
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DT 01-MAY-2000 (TREMblrel. 15, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

RP SEQUENCE FROM N.A.

RC STRAIN=CS2184364; PubMed=10537472;

RA Mue A., Quiñones-Mateu M.E., Domingo E., Soriano V.,

*Phylogeny of HIV type 1 group O isolates based on env gene

RT sequences. Hum. Retroviruses 15:769-773(1999).

DR EMBL: AF081817; AA04129.1; "

DR INTERPRO: IPR000328; "

KM Envelope Protein. 1

FT NON_TER 146

SO SEQUENCE 146 AA: 16639 MW: B193930C080F60FC CRC64:

Query Match 93.5% Score 87: DB 12: Length 146:
Best Local Similarity 93.8% Pred. No. 6.9e-07:
Matches 15: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 1 LNSMCKGRVLCYTS 16
DB 69 LNSMCKGRVLCYTS 84

RESULT 13

ID 091EC3 PRELIMINARY: PRT: 213 AA.

AC 091EC3
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

RP SEQUENCE FROM N.A.

RC STRAIN=96CF09;

RA Rouques P., Robertson D., Sandrine S., Christel D., Francois S.,
Philippe M.,

*Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."

RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ33396; CAB96245.1; "

FT NON_TER 213

FT NON_TER 213

SO SEQUENCE 213 AA: 24612 MW: 8FE10970A233434 CRC64:

Query Match 93.5% Score 87: DB 12: Length 213:
Best Local Similarity 93.8% Pred. No. 9.8e-07:
Matches 15: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 1 LNSMCKGRVLCYTS 16
DB 45 LNSMCKGRVLCYTS 60

RESULT 14

ID 091E96 PRELIMINARY: PRT: 214 AA.

AC 091E96
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

RP SEQUENCE FROM N.A.

RC STRAIN=YBR49;

RA Rouques P., Robertson D., Sandrine S., Christel D., Francois S.,
Philippe M.,

*Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."

RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ256424; CAB96242.1; "

FT NON_TER 214

FT NON_TER 214

SO SEQUENCE 214 AA: 25052 MW: B216C13A24C45A5E CRC64:

Query Match 93.5% Score 87: DB 12: Length 214:
Best Local Similarity 93.8% Pred. No. 9.9e-07:

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LINSWCKGRLVCYTS 16
 Db 45 LINSWCKGRLVCYTS 60

RESULT 15

Q9IEA5 PRELIMINARY: PRT: 216 AA.
 AC Q9IEA5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE GP41 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RX 11
 ST SEQUENCE FROM N.A.
 RA Philippe M.; Robertson D.; Sandrine S.; Francois S.;
 RT *Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.*;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AV236415; CAB96263.1;
 FT
 FT NON-TER 1 216
 FT / 1
 SQ SEQUENCE 216 AA; 25003 MW: 0A5AC218BPA8932 CRC64;

Query Match 93.5%; Score 87; DB 12; Length 216;
 Best Local Similarity 93.8%; Pred. No. 1e-06;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LINSWCKGRLVCYTS 16
 Db 42 LINSWCKGRLVCYTS 57

Search completed: March 22, 2001, 10:00:45
 Job time: 324 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:50:45 ; Search time 29.4 seconds

(without alignments)
17,575 Million cell updates/sec

Title: US-09-147-362-10

Perfect score: 93

Sequence: 1 LLNSMCKGRLYCYTS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.39:*

Result No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	65	67.7	857	ENV_HV2KR	P1281 chimpanzee
2	63	67.7	856	ENV_HV2K2	P3252 human immun
3	60	64.5	712	ENV_HV2S2	P3252 human immun
4	60	64.5	843	ENV_HV1Y2	P3252 human immun
5	60	64.5	846	ENV_HV2S8	P3252 human immun
6	60	64.5	847	ENV_HV1S1	P3252 human immun
7	60	64.5	847	ENV_HV1S1	P3252 human immun
8	60	64.5	847	ENV_HV1S1	P3252 human immun
9	60	64.5	851	ENV_HV1B8	P04582 human immun
10	60	64.5	851	ENV_HV1B8	P04582 human immun
11	60	64.5	851	ENV_HV1B8	P04582 human immun
12	60	64.5	852	ENV_HV1B8	P04582 human immun
13	60	64.5	853	ENV_HV1S3	P19551 human immun
14	60	64.5	853	ENV_HV1S3	P19551 human immun
15	60	64.5	853	ENV_HV1S3	P19551 human immun
16	60	64.5	855	ENV_HV1A2	P03378 human immun
17	60	64.5	855	ENV_HV1A2	P03378 human immun
18	60	64.5	855	ENV_HV1A2	P03378 human immun
19	60	64.5	855	ENV_HV1A2	P03378 human immun
20	60	64.5	856	ENV_HV1A2	P03378 human immun
21	60	64.5	856	ENV_HV1A2	P03378 human immun
22	60	64.5	856	ENV_HV1A2	P03378 human immun
23	60	64.5	856	ENV_HV1A2	P03378 human immun
24	60	64.5	856	ENV_HV1A2	P03378 human immun
25	60	64.5	856	ENV_HV1A2	P03378 human immun
26	60	64.5	856	ENV_HV1A2	P03378 human immun
27	60	64.5	856	ENV_HV1A2	P03378 human immun
28	60	64.5	856	ENV_HV1A2	P03378 human immun
29	60	64.5	856	ENV_HV1A2	P03378 human immun
30	60	64.5	856	ENV_HV1A2	P03378 human immun
31	60	64.5	856	ENV_HV1A2	P03378 human immun
32	60	64.5	856	ENV_HV1A2	P03378 human immun
33	60	64.5	856	ENV_HV1A2	P03378 human immun

ALIGNMENTS

Result No.	Score	% Query Match	Length	ID	Description
34	60	64.5	868	ENV_HV1C4	P05879 human immun
35	60	64.5	868	ENV_HV1C4	P12492 simian immun
36	60	64.5	868	ENV_HV1C4	P12492 simian immun
37	60	64.5	868	ENV_HV1C4	P12492 simian immun
38	60	64.5	868	ENV_HV1C4	P12492 simian immun
39	60	64.5	868	ENV_HV1C4	P12492 simian immun
40	60	64.5	868	ENV_HV1C4	P12492 simian immun
41	60	64.5	868	ENV_HV1C4	P12492 simian immun
42	60	64.5	868	ENV_HV1C4	P12492 simian immun
43	60	64.5	868	ENV_HV1C4	P12492 simian immun
44	60	64.5	868	ENV_HV1C4	P12492 simian immun
45	60	64.5	868	ENV_HV1C4	P12492 simian immun

FT CARBOHYD 142 142 N-LINKED (GLCNGC . . .) (POTENTIAL)
 FT CARBOHYD 182 182 N-LINKED (GLCNGC . . .) (POTENTIAL)
 FT CARBOHYD 183 183 N-LINKED (GLCNGC . . .) (POTENTIAL)
 FT CARBOHYD 196 196 N-LINKED (GLCNGC . . .) (POTENTIAL)
 FT CARBOHYD 228 228 N-LINKED (GLCNGC . . .) (POTENTIAL)
 FT CARBOHYD 231 231 N-LINKED (GLCNGC . . .) (POTENTIAL)
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 FT CARBOHYD 355 355 N-LINKED (GLCNGC . . .) (POTENTIAL)
 FT CARBOHYD 390 390 N-LINKED (GLCNGC . . .) (POTENTIAL)
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 FT CARBOHYD 627 627 N-LINKED (GLCNGC . . .) (POTENTIAL)
 SEQUENCE 856 AA; 98665 MW; A53BD0A72E8B01D6 CRC64;

Query Match 67.7%; Score 63; DB 1; Length 856;
 Best Local Similarity 73.3%; Pred. No. 0.013;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 LNSMCKGRLGYCYS 16
 Db 583 LNSMCKGRLGYCYS 597

RESULT 4
 ID ENV_HV2S2 STANDARD; PRT; 712 AA.
 AC B32536;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
 DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
 OS Human immunodeficiency virus type 2 (isolate ST/24_1C42) (HIV-2).
 CC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92260681; PubMed-1583738;
 Mulligan M.J., Yamshchikov G.V., Ritter G.D., Jr., Gao F., Jin M.J.,
 Nall C.D., Spies C.P., Hahn B.H., Compans R.W.,
 Cytoplasmic domain truncation enhances fusion activity by the
 exterior glycoprotein complex of human immunodeficiency virus type 2
 in vitro. 66-3973, J. Virol. 73(1992).

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EMBL: M66924; AAA43938.1; -
 PIR: A42535; VCL354.
 INTERPRO: IPR000328; -
 DR PFM: PFM0516; GRI10; 1.
 DR PFM: PFM0516; GRI10; 1.
 KW Aids; Coat Protein; Glycoprotein; Glycoprotein; Transmembrane;
 FT SIGNAL 1 19 ENV POLYPEPTIDE.
 FT CHAIN 20 712 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 20 495

FT CHAIN 496 712 TRANSMEMBRANE GLYCOPROTEIN.
 FT CARBOHYD 675 694 POTENTIAL.
 FT CARBOHYD 696 696 N-LINKED (GLCNGC . . .) (POTENTIAL)
 FT CARBOHYD 758 758 N-LINKED (GLCNGC . . .) (POTENTIAL)
 FT CARBOHYD 759 759 N-LINKED (GLCNGC . . .) (POTENTIAL)
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 FT CARBOHYD 614 614 N-LINKED (GLCNGC . . .) (POTENTIAL)
 FT CARBOHYD 618 618 N-LINKED (GLCNGC . . .) (POTENTIAL)
 SEQUENCE 712 AA; 81723 MW; 4BC7F3C03D3C3469 CRC64;

Query Match 64.5%; Score 60; DB 1; Length 712;
 Best Local Similarity 66.7%; Pred. No. 0.032;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 LNSMCKGRLGYCYS 16
 Db 586 LNSMCKGRLGYCYS 600

RESULT 5
 ID ENV_HV12 STANDARD; PRT; 843 AA.
 AC B35961;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
 DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
 CC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93021387; PubMed-1404605;
 Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
 Shaw G.M.;
 Complete nucleotide sequence, genome organization, and biological
 properties of human immunodeficiency virus type 1 in vivo: evidence
 for limited defectiveness and complementation.
 J. Virol. 66:6597-6600(1992).

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DR EMBL: M93258.1; NOT_ANNOTATED_CDS.
DR PIR: H44001. H44001.
DR INTERPRO: IPR000328.
DR INTERPRO: IPR000777.
DR PFM: PF00516; GP120. 1.
DR PFM: PF00517; GP41. 1.
DR AIDs: Coat protein; Glycoprotein; Transmembrane;
  Signal.
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RN SEQUENCE FROM N.A.
RA MEDLINE:8918461; PubMed:2648404;
RA Franchini G., Fargnoli K.A., Giombini F., Jagodzinski L., de Rossi A.,
RA Bosch M., Biberfeld G., Fenyo A.M., Albert J., Gallo R.C.,
RA Wong-Staal F.; biological characterization of a replication competent
RA Human immunodeficiency virus type 2 (HIV-2) proviral clone.
RA Proc Natl Acad Sci U S A 86:2433-2437(1989).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to contact@isb-sib.ch).
DR EMBL: J04498; AAB00752.1;
DR HIV: J04498; ENV5218Y.
DR INTERPRO: IPR000328.
DR INTERPRO: IPR000777.
DR PFM: PF00516; GP120. 1.
DR PFM: PF00517; GP41. 1.
DR AIDs: Coat protein; Glycoprotein; Transmembrane;
  Signal.
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FT CAROHD 350 350 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 356 356 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 380 380 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 386 386 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 390 390 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 400 400 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 438 438 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 450 450 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 452 452 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 607 607 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 616 616 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 628 628 N-LINKED (GLCNC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA; 96466 MW; CDIE3JD73AASBCAE CRC64;

Query Match 64.5%; Score 60; DB 1; Length 847;
Best Local Similarity 56.2%; Pred. No. 0.038; 4; Indels 0; Gaps 0;
Matches 3; Conservative 3; Mismatches 4;

1 L1NSMCGSRGRCYCTS 16
1 L1NSMCGSRGRCYCTS 16
583 L1G1MCGSKLICITTT 598

RESULT 9
ENV_HIV198 STANDARD; PRT: 851 AA.
AD P04582
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS human immunodeficiency virus type 1 (8H isolate) (HIV-1).
OU HIV/AIDS; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-0511123; Pubmed-2578615;
RA Ralner L., Haseltine W., Patarca R., Llyak K.J., Starcich B.R.,
RA Joseph S.F., Doran E.R., Ratajski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Laubenberg J.A., Pappas T.S., Ghayee J., Chang N.T., Gallo R.C.,
RA "Long-Steady" peptide sequence of the AIDS virus, HIV-III.*
RL Nature 313:277-284(1985).
CC -----
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CC modified and this statement is not removed, usage by and for commercial
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CC -----
CC EMBL: K02011; AAA4661.1;
DR HIV: K02011; ENVBH8.
DR INTERPRO: IP0000328;
DR INTERPRO: IP000777;
DR PFM: PF00516; GP120; 1.
DR PFM: PF00517; GP41; 1.
KM Signal Coat Protein, Glycoprotein; Glycoprotein; Transmembrane;
FT SIGNAL 1 30
FT CHAIN 1 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 507 851 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFD 54 74 BY SIMILARITY.
FT DISULFD 119 205 BY SIMILARITY.
FT DISULFD 126 196 BY SIMILARITY.
FT DISULFD 231 257 BY SIMILARITY.
FT DISULFD 238 240 BY SIMILARITY.
FT DISULFD 238 240 BY SIMILARITY.
FT DISULFD 331 331 BY SIMILARITY.

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FT DISULFD 378 440 BY SIMILARITY.
FT DISULFD 385 413 BY SIMILARITY.
FT CAROHD 88 88 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 136 136 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 141 141 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 156 156 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 160 160 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 186 186 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 197 197 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 237 237 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 234 234 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 241 241 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 262 262 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 276 276 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 295 295 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 301 301 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 332 332 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 339 339 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 359 359 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 386 386 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 392 392 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 401 401 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 443 443 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 458 458 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 606 606 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 611 611 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 620 620 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 630 630 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 669 669 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 745 745 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CAROHD 811 811 N-LINKED (GLCNC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C908577895F1 CRC64;

Query Match 64.5%; Score 60; DB 1; Length 851;
Best Local Similarity 56.2%; Pred. No. 0.038; 4; Indels 0; Gaps 0;
Matches 3; Conservative 3; Mismatches 4;

1 L1NSMCGSRGRCYCTS 16
1 L1NSMCGSRGRCYCTS 16
587 L1G1MCGSKLICITTTA 602

RESULT 10
ENV_HIV21 STANDARD; PRT: 851 AA.
AD P1755;
DT 01-NOV-1990 (Rel. 15, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN human immunodeficiency virus type 2 (isolate D194) (HIV-2).
OU HIV/AIDS; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91045094; Pubmed-2235509;
RA Kneisel H., Kreutz R., Ruesamen-Waligmann H.;
RA "Nucleotide sequence of HIV-2D194, an isolate from a Gambian case of
RA "HIV-2, which showed excellent growth in macrophages."
RL Nucleic Acids Res. 18:6142-6142(1990).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89184631; Pubmed-2467304;
RA Kneisel H., von Briesen A., Dietrich U., Adamski M., Mix D.,
RA Blesert L., Kreutz R., Immelmann A., Henck C., Melchner C.,
RA "Molecular cloning of two west African human immunodeficiency virus
RA type 2 isolates that replicate well in macrophages: a Gambian
RA isolate, from a patient with neurologic acquired immunodeficiency
RA syndrome, and a highly divergent isolate."
RL Proc. Natl. Acad. Sci. U.S.A. 86:2383-2387(1989).

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Db	Qy	Matches	Conservative	Mismatches	Indels	Gaps
583	2	583	10	2	3	0
597	16	597	10	2	3	0

Query Match 64.5%; Score 60; DB 1; Length 851;
 Best Local Similarity 66.7%; Pred. No. 0.038;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 12

ID	EN- <u>HVJBN</u>	STANDARD:	PRT:	852 AA.
EN-	ENV-HVJBN			
NC	P12498	-1989 (Ref. 12)		(Created)
CC	01-OCT-1989 (Ref. 12)			(sequence update)
DT	15-JUL-1999 (Ref. 38)			Last annotation update)
DE	ENVELOPE POLYPEPTIDE PROTEIN PRONUCLEON (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (JR isolate) (HIV-1).			
OC	Viruses; Retroviridae; Lentivirinae.			
CC	11			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=89085613			pubmed=2789516;
RA	Amond R., Payer R., Shrivastava A., Nayyar S., Gardner M., Luciw P., Dandekar S.;			
RT	"Biological and molecular characterization of human immunodeficiency virus (HIV-1JR) from the brain of a patient with progressive dementia."			
RT	Virology 168:79-89(1999).			
RT	-1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute and the EMBL Outstation at the European Bioinformatics Institute. This project has no way of being used by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.jab-slb.ch/announcements/ or send an email to license@slb-sb.ch).			
CC	EMBL: M2099; AAA44221.1; .			
DR	HIT: A2109; ECLABR.			
DR	HIT: A2109; ECLABR.			
DR	INTERPRO: IPR000328.			
DR	INTERPRO: IPR000777; .			
DR	PFAM: PF00516; GP120_1.			
KW	AIDS; Coat protein; polyprotein; glycoprotein; Transmembrane; Signal.			
NM	SIGNAL.			
FT	1	30		
FT	CHAIN	507		EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	DISULFID	508	82	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	5	92	
FT	DISULFID	119	205	BY SIMILARITY.
FT	DISULFID	126	195	BY SIMILARITY.
FT	DISULFID	131	155	BY SIMILARITY.
FT	DISULFID	218	247	BY SIMILARITY.
FT	DISULFID	228	239	BY SIMILARITY.
FT	DISULFID	296	330	BY SIMILARITY.
FT	DISULFID	376	439	BY SIMILARITY.
FT	CARBOHYD	383	412	BY SIMILARITY.
FT	CARBOHYD	389	469	BY SIMILARITY.
FT	CARBOHYD	135	135	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	138	138	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	154	154	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	158	158	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	197	197	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	234	234	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	241	241	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	262	262	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	266	266	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	285	285	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	301	301	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	331	331	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	354	354	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	360	360	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	384	384	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	390	390	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	396	396	N-LINKED (GLCNAC.) (POTENTIAL).
FT	CARBOHYD	400	400	N-LINKED (GLCNAC.) (POTENTIAL).

[illegible]

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Query Match      64.5%  Score 60:  DB 1:  Length 832;
Best local similarity 56.2%,  Pred. NO. 0.038;
Matches 9;  Conservative 3;  Mismatches 4;  Indels 0;  Gaps 0;

QY      1  LLSNCKGKRLVCVTS 16
      || || | | | | | |
DB      588  LLSGWSGKRLVCIT 603

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SEQUENCE FROM N.A.
MEDLINE-90317877: Pubmed-1695254:
Stevenson M., Haggerty S., Iamonica C., Mann A.M., Meiler C.,
Waslak A.:
Cloning and characterization of human immunodeficiency virus type 1
variants diminished in the ability to induce syncytium-independent
cytolysis." J. Virol. 64:3792-3803(1990).

or send an email to license@lsb.sib.ch).

```

Query Match      64.5%  Score 60: DB 1: Length 853;
Best Local Similarity 56.2%: Pctd No. 0.008;
Matches 9: Conservative 3: Mismatches 4: Indels 0: Gaps 0:
QY      1 LINSBCKGRVCTYS 16
      |||||.:.:.:.:
Db      590 LLSINGSKALICTTA 605

```

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
[1]

Gencore version 4.5
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:50:42 ; Search time 57.2 Seconds

(without alignments)
18,993 Million cell updates/sec

Title: US-09-147-362-10

Perfect score: 93

Sequence: 1 ILNMQCKGRLCYTS 16

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 195891 seqs, 67900655 residues

tal number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	90	86.0	877	2	S49197
2	79	86.0	877	2	S49197
3	78	86.0	877	2	S49197
4	64	68.8	855	2	S21990
5	63	67.7	357	2	S21990
6	63	67.7	357	2	S21990
7	63	67.7	358	2	S22002
8	63	67.7	358	2	S70418
9	63	67.7	854	1	VCLJST
10	63	67.7	854	1	VCLJST
11	63	67.7	854	1	VCLJST
12	62	66.7	358	2	S70417
13	60	64.5	151	2	S30458
14	60	64.5	151	2	S30458
15	60	64.5	151	2	S30448
16	60	64.5	151	2	S30448
17	60	64.5	151	2	S30452
18	60	64.5	151	2	S30452
19	60	64.5	151	2	S30450
20	60	64.5	151	2	S30457
21	60	64.5	151	2	S30456
22	60	64.5	151	2	S30454
23	60	64.5	151	2	S30454
24	60	64.5	357	2	S22006
25	60	64.5	357	2	S21994
26	60	64.5	357	2	S22004
27	60	64.5	357	2	S21996
28	60	64.5	357	2	S21992
29	60	64.5	357	2	S70419

30	60	64.5	357	2	S70421	envelope protein g
31	60	64.5	358	2	S21998	envelope protein g
32	60	64.5	358	2	S70425	envelope protein g
33	60	64.5	366	2	B41565	env polypeptide
34	60	64.5	443	2	C41621	env polypeptide M
35	60	64.5	445	2	A41621	env polypeptide D
36	60	64.5	454	2	B41621	env polypeptide B
37	60	64.5	712	1	VCLJST	env polypeptide pr
38	60	64.5	813	1	H40001	env polypeptide pr
39	60	64.5	847	2	S13289	env polypeptide pr
40	60	64.5	847	2	S13289	env polypeptide pr
41	60	64.5	851	2	S12159	env polypeptide pr
42	60	64.5	852	1	VCLJST	env polypeptide - huma
43	60	64.5	852	1	VCLJST	env polypeptide pr
44	60	64.5	852	2	T12016	envelope glycoprotein
45	60	64.5	853	2	S54384	envelope polypeptide

ALIGNMENTS

RESULT 1

S49197 envelope protein precursor - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence-revision 24-Jul-1997 #text-change 26-Aug-1999

C:Accession: S49197

A:Accession: S49197

A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: d

A:Reference number: S49197

A:Accession: S49197

A:Molecule type: DNA

A:Residues: 1-877 <CH>

A:Cross-references: EMBL:X80020; NID:9510516; PIDN:CA56323.1; PID:9510517

A:Experimental source: Isolate VAO

C:Supernatant: supernatant from cell culture

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-535/Product: coat protein gp120 #status predicted <CP1>

F:536-877/Product: coat protein gp41 #status predicted <CP2>

F:698-716/Domain: transmembrane #status predicted <TM>

F:59,88,139,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,4

Query Match Best Local Similarity 86.0% Score 80. DB 2. Length 877:

Matches 13: Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 607 ILNMQCKGRLCYTS 16

QY 1 ILNMQCKGRLCYTS 16

gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 03-May-1994 #sequence-revision 03-May-1994 #text-change 07-May-1999

C:Accession: A53034

J:Vanden Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborght, B.; van der Groe

A:Reference number: A53034

A:Accession: A53034

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-863 <VAN>

A:Cross-references: GB:102587

C:Superfamily: type B retrovirus env polypeptide

C:Keywords: polypeptide

Query Match 84.9% Score 79; DB 2; Length 663;
 Best Local Similarity 81.2% Pred. No. 0.0002;
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 LNSMCGKGRLYCYTS 16
 Db 594 LLSMCGKGRLYCYTS 609

RESULT 3

S52930
 GP41 ENV protein - human immunodeficiency virus type 1 (fragment)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C>Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #textL_change 26-Aug-1999
 C:Accession: S52930
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Haecke, W.
 submitted to the EMBL Data Library, July 1991
 A:Description: A novel HIV-1 O strain illustrates the diversity of the O group.
 A:Reference number: S52929
 A:Accession: S52930
 A:Molecule type: preliminary
 A:Residues: 1-104 <COH>
 A:Cross-references: EMBL:X84328; NID:g695526; PIDN:CAA59066.1; PID:g695527
 C:Superfamily: type E retrovirus env polyprotein

Query Match 80.6% Score 75; DB 2; Length 104;
 Best Local Similarity 68.8% Pred. No. 0.00014;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 LNSMCGKGRLYCYTS 16
 Db 45 LLSMCGKGRLYCYTS 60

RESULT 4

A45713
 Env transmembrane protein gp43 - human immunodeficiency virus type 2
 C:Species: human immunodeficiency virus type 2, HIV-2
 C>Date: 04-Mar-1994 #sequence_revision 18-Nov-1994 #textL_change 12-Apr-1995
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Haecke, W.
 submitted to the EMBL Data Library, July 1991
 A:Title: Delineating features of an infectious molecular clone of the highly divergent
 A:Reference number: A45713; NID:93124535
 A:Accession: A45713
 A:Molecule type: DNA
 A:Status: preliminary; not compared with conceptual translation
 A:Residues: 1-855 <DAR>
 A:Reference number: UCL
 A:Note: Recombinant source: UCL from NCBI backbone (NCBI:122362)
 C:Superfamily: type E retrovirus env polyprotein

Query Match 68.8% Score 64; DB 2; Length 855;
 Best Local Similarity 68.8% Pred. No. 0.037;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 LNSMCGKGRLYCYTS 16
 Db 594 LLSMCGKGRLYCYTS 609

RESULT 5

S21990
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #textL_change 26-Aug-1999
 C:Accession: S21990
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Haecke, W.
 submitted to the EMBL Data Library, July 1991
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi

A:Reference number: S21990
 A:Accession: S21990
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <STE>
 A:Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176
 C:Superfamily: type E retrovirus env polyprotein

Query Match 67.7% Score 63; DB 2; Length 357;
 Best Local Similarity 62.5% Pred. No. 0.026;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 LNSMCGKGRLYCYTS 16
 Db 93 LLSMCGKGRLYCYTS 108

RESULT 6

S70423
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 20) (frag
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Variety: patient 20
 C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #textL_change 26-Aug-1999
 C:Accession: S70423
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
 A:Reference number: S70417; NID:92144209
 A:Accession: S70423
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <STE>
 A:Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176
 C:Superfamily: type E retrovirus env polyprotein

Query Match 67.7% Score 63; DB 2; Length 357;
 Best Local Similarity 62.5% Pred. No. 0.026;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 LNSMCGKGRLYCYTS 16
 Db 93 LLSMCGKGRLYCYTS 108

RESULT 7

S22002
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #textL_change 26-Aug-1999
 C:Accession: S22002
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Haecke, W.
 submitted to the EMBL Data Library, July 1991
 A:Title: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
 A:Reference number: S21990
 A:Accession: S22002
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-358 <STE>
 A:Cross-references: EMBL:X61357; NID:g60186; PIDN:CAA43616.1; PID:g60187
 C:Superfamily: type E retrovirus env polyprotein

Query Match 67.7% Score 63; DB 2; Length 358;
 Best Local Similarity 62.5% Pred. No. 0.026;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 LNSMCGKGRLYCYTS 16
 Db 94 LLSMCGKGRLYCYTS 109

RESULT 8
S70418
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3L) (fragment
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3L
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
R:Steuiler, H. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro-
A:Reference number: S70417; MUID:92144209
A:Accession: S70418
A:Status: preliminary
A:Gene: env
A:Molecule type: DNA
A:Residues: 1-358 <STR>
C:Cross-references: EMBL:X61352; NID:960186; PIDD:CAA43616.1; PID:960187
C:Superfamily: type B retrovirus env polypeptide

Query Match 67.7%; Score 63; DB 2; Length 358;
Best Local Similarity 62.5%; Pred. No. 0.026;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 LNSMCKGRLVCTYS 16
DB 94 LLIWCKGRLVCTYH 109

RESULT 9
env polypeptide precursor - simian immunodeficiency virus SIVcpz
N:Alternate names: coat polypeptide
A:Accession: S22000
C:Species: simian immunodeficiency virus SIVcpz
A:Note: host pan troglodytes (chimpanzee)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: S09390
R:Huett, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A:Accession: S09390
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-854 <HUS>
A:Cross-references: EMBL:X52154; NID:958866; PIDD:CAA36407.1; PID:958874
C:Gene: env
C:Superfamily: type E retrovirus env polypeptide

F:1-30/Domains: signal sequence, glycoprotein; Immunodeficiency; polyprot
F:31-500/Product: coat protein gp120 status predicted <SIG>
F:501-854/Product: coat protein gp41 status predicted <CP2>
F:501-517/Domains: transmembrane status predicted <TM1>
F:675-693/Domains: transmembrane status predicted <TM2>
F:805-821/Domains: transmembrane status predicted <TM3>
F:1134-140,143,154,158,166,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45

Query Match 67.7%; Score 63; DB 1; Length 854;
Best Local Similarity 56.2%; Pred. No. 0.053;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 LNSMCKGRLVCTYS 16
DB 582 LLIWCKGRLVCTYH 397

RESULT 10
VCLJST
env polypeptide precursor - human immunodeficiency virus type 2 (isolate ST)
N:Alternate names: coat polypeptide
A:Accession: S70417
A:Status: surface glycoprotein gp120; transmembrane glycoprotein gp41

C:Species: human immunodeficiency virus type 2, HIV-2
A:Note: host Homo sapiens (man)
C:Date: 20-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1994
C:Accession: S70417
R:Kumar, P.; Hui, H.; Kappes, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.
J. Virol. 64, 890-901, 1990
A:Title: Molecular characterization of an attenuated human immunodeficiency virus typ
A:Reference number: A33943; MUID:90112662
A:Accession: H33943
A:Molecule type: genomic RNA
A:Residues: 1-859 <HUS>
C:Cross-references: EMBL:M86924
C:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-19/Domains: signal sequence status predicted <SIG>
F:20-859/Product: env polypeptide status predicted <ENV>
F:20-859/Product: surface glycoprotein gp120 status predicted <SGD>
F:507-523/Product: transmembrane glycoprotein gp41 status predicted <TGD>
F:675-694/Domains: transmembrane status predicted <TM1>
F:36,69,78,113,119,131,137,145,160,173,186,200,222,235,242,266,272,283,294,304,359,39

Query Match 67.7%; Score 63; DB 1; Length 859;
Best Local Similarity 66.7%; Pred. No. 0.053;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 LNSMCKGRLVCTYS 16
DB 586 LLIWCKGRLVCTYH 600

RESULT 11
S22000
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C:Accession: S22000
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete
A:Accession: S21990
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <STR>
A:Cross-references: EMBL:X61351
C:Superfamily: type E retrovirus env polypeptide

Query Match 66.7%; Score 62; DB 2; Length 358;
Best Local Similarity 66.7%; Pred. No. 0.037;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 LNSMCKGRLVCTYS 15
DB 94 LLIWCKGRLVCTYH 108

RESULT 12
S70417
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragm
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3B
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Accession: S70417; MUID:92144209

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-358 <STD>
 A:Cross-references: EMBL:X61351; NID:60184; PIDD:CAA3614.1; PID:60185
 C:Superfamily: type E retrovirus env polyprotein

Query Match 66.7%; Score 62; DB 2; Length 358;
 Best Local Similarity 66.7%; Pred. No. 0.037;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 LNSMCKGRLVCTT 15
 Db 94 LNSMCKGRLVCTT 108

RESULT 13
 env protein - human immunodeficiency virus type 2 (fragment)

Species: human immunodeficiency virus type 2, HIV-2
 C:Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
 C:Accession: S30448; S30449; S30480; S30481
 R:Go, F.: Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
 Nature 358, 495-499, 1992
 A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
 A:Reference number: S30448; M0ID:92350299
 A:Accession: S30458
 A:Molecule type: nucleic acid
 A:Residues: 1-151 <GMO>
 A:Cross-references: EMBL:M87142
 R:Go, F.: Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
 submitted to the EMBL Data Library, December 1992
 A:Description: Human infection by genetically diverse SIV(SM)-related HIV-2 in west Africa
 A:Reference number: S30460
 A:Accession: S30477
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-151 <GA2>
 A:Cross-references: EMBL:M87141
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: coat protein; glycoprotein

Query Match 64.5%; Score 60; DB 2; Length 151;
 Best Local Similarity 66.7%; Pred. No. 0.036;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 LNSMCKGRLVCTT 16
 Db 37 LNSMCKAFVCHT 51

RESULT 14
 env protein - human immunodeficiency virus type 2 (fragment)
 C:Species: human immunodeficiency virus type 2, HIV-2
 C:Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
 C:Accession: S30459
 R:Go, F.: Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
 Nature 358, 495-499, 1992
 A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
 A:Reference number: S30448; M0ID:92350299
 A:Accession: S30459
 A:Status: translation not shown
 A:Molecule type: nucleic acid
 A:Residues: 1-151 <GMO>
 A:Cross-references: EMBL:M87143
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: coat protein; glycoprotein

Query Match 64.5%; Score 60; DB 2; Length 151;
 Best Local Similarity 66.7%; Pred. No. 0.036;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 LNSMCKGRLVCTT 16
 Db 37 LNSMCKAFVCHT 51

RESULT 15
 env protein - human immunodeficiency virus type 2 (fragment)
 C:Species: human immunodeficiency virus type 2, HIV-2
 C:Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
 C:Accession: S30448; S30449; S30480; S30481
 R:Go, F.: Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.
 Nature 358, 495-499, 1992
 A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
 A:Reference number: S30448; M0ID:92350299
 A:Accession: S30448
 A:Molecule type: nucleic acid
 A:Residues: 1-151 <GMO>
 A:Cross-references: EMBL:M87069
 A:Experimental source: FOENVA13
 A:Accession: S30449
 A:Molecule type: translation not shown
 A:Residues: 1-151 <GMO>
 A:Cross-references: EMBL:M87071
 R:Go, F.: Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.
 submitted to the EMBL Data Library, December 1992
 A:Description: Human infection by genetically diverse SIV(SM)-related HIV-2 in west Afr
 A:Reference number: S30460
 A:Accession: S30480
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-151 <GA2>
 A:Cross-references: EMBL:M87085
 A:Accession: S30481
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-151 <GA2>
 A:Cross-references: EMBL:M87076
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: coat protein; glycoprotein

Query Match 64.5%; Score 60; DB 2; Length 151;
 Best Local Similarity 66.7%; Pred. No. 0.036;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 LNSMCKGRLVCTT 16
 Db 37 LNSMCKAFVCHT 51

Search completed: March 22, 2001, 09:53:44
 Job time: 182 sec

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GenCore version 4.5
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OK protein - protein search, using sw model

Run on: March 22, 2001, 09:50:42 : Search time 46.96 Seconds
(without alignments)
6,118 Million cell updates/sec

Title: US-09-147-362-10

Sequence: 1 LNSMCKGRLVCTYS 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Maximum number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database: Issued Patents, AA.*
1: /cgn2.6/p/odata/2/1aa/58.COMB.pep.*
2: /cgn2.6/p/odata/2/1aa/58.COMB.pep.*
3: /cgn2.6/p/odata/2/1aa/6.COMB.pep.*
4: /cgn2.6/p/odata/2/1aa/PCITUS.COMB.pep.*
5: /cgn2.6/p/odata/2/1aa/BACKFILES1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	100.0	33	US-09-433-4280-5	Sequence 25, Appl
2	93	100.0	33	US-09-433-4280-5	Sequence 25, Appl
3	93	100.0	40	US-08-894-659-38	Sequence 13, Appl
4	93	100.0	40	US-08-894-659-38	Sequence 13, Appl
5	91	97.8	33	US-09-433-4280-30	Sequence 30, Appl
6	91	97.8	40	US-08-894-659-36	Sequence 36, Appl
7	87	93.5	33	US-09-433-4280-4	Sequence 4, Appl
8	87	93.5	33	US-09-433-4280-7	Sequence 7, Appl
9	87	93.5	33	US-09-433-4280-5	Sequence 15, Appl
10	87	93.5	41	US-08-894-659-66	Sequence 66, Appl
11	86	92.5	23	US-09-433-4280-59	Sequence 59, Appl
12	86	92.5	23	US-09-433-4280-60	Sequence 60, Appl
13	86	92.5	23	US-09-433-4280-61	Sequence 61, Appl
14	86	92.5	28	US-09-433-4280-62	Sequence 62, Appl
15	86	92.5	30	US-09-433-4280-63	Sequence 63, Appl
16	86	92.5	30	US-09-433-4280-69	Sequence 69, Appl
17	86	92.5	33	US-09-433-4280-8	Sequence 3, Appl
18	86	92.5	33	US-09-433-4280-8	Sequence 3, Appl
19	86	92.5	33	US-09-433-4280-14	Sequence 14, Appl
20	86	92.5	33	US-09-433-4280-16	Sequence 16, Appl
21	86	92.5	33	US-09-433-4280-29	Sequence 29, Appl
22	86	92.5	35	US-09-433-4280-64	Sequence 64, Appl
23	86	92.5	41	US-08-894-659-67	Sequence 67, Appl
24	86	92.5	149	US-09-433-4280-57	Sequence 57, Appl
25	86	92.5	210	US-08-912-129A-54	Sequence 54, Appl
26	86	92.5	27	US-09-433-4280-26	Sequence 26, Appl
27	86	92.5	27	US-09-433-4280-26	Sequence 26, Appl
28	86	92.5	243	US-08-912-129A-48	Sequence 48, Appl

29	86	92.5	358	3	US-09-433-4280-58	Sequence 58, Appl
30	86	92.5	373	2	US-08-912-129A-52	Sequence 52, Appl
31	86	92.5	439	3	US-09-433-4280-57	Sequence 57, Appl
32	86	92.5	460	2	US-08-912-129A-60	Sequence 60, Appl
33	86	92.5	490	2	US-08-912-129A-50	Sequence 50, Appl
34	86	92.5	618	2	US-08-912-129A-54	Sequence 54, Appl
35	86	92.5	873	2	US-08-912-129A-61	Sequence 61, Appl
36	85	91.4	33	3	US-09-433-4280-10	Sequence 10, Appl
37	85	91.4	33	3	US-09-433-4280-18	Sequence 18, Appl
38	84	90.3	33	3	US-09-433-4280-27	Sequence 27, Appl
39	84	90.3	33	3	US-09-433-4280-27	Sequence 27, Appl
40	84	90.3	40	3	US-08-894-659-47	Sequence 47, Appl
41	84	90.3	40	3	US-08-894-659-40	Sequence 40, Appl
42	83	89.2	33	3	US-09-433-4280-12	Sequence 12, Appl
43	83	89.2	33	3	US-09-433-4280-22	Sequence 22, Appl
44	83	89.2	33	3	US-09-433-4280-26	Sequence 26, Appl
45	83	89.2	33	3	US-09-433-4280-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-433-4280-6
Sequence 6, Application US/094334280
Patent No. 6149910
GENERAL INFORMATION:
INVENTOR: Zheng, J. Robert J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 33
LENGTH: 33
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-4280-6

Query Match 100.0% Score 93: DB 3: Length 33:
Best Local Similarity 100.0% Pred. No. 3.7e-08:
Matches 16: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 14 LNSMCKGRLVCTYS 29
DB 14 LNSMCKGRLVCTYS 29
RESULT 2
US-09-433-4280-25
Sequence 25, Application US/094334280
Patent No. 6149910
GENERAL INFORMATION:
INVENTOR: Zheng, J. Robert J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 25
LENGTH: 33
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-4280-25
Query Match 100.0% Score 93: DB 3: Length 33:
Best Local Similarity 100.0% Pred. No. 3.7e-08:

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSNMGCKGRLVCYTS 16
Db 19 LLSNMGCKGRLVCYTS 29

RESULT 3
US-08-894-699-39
Sequence 39, Application US/08894699
Patent No. 6030769

GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENIOR
APPLICANT: LOUSSERT-ARANA, IBITISSAM
APPLICANT: LY, THOI-DIUNG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUBSTADT,
P.C.
STREET: 1753 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC COMPATIBLE
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894, 699
FILING DATE: 01-DEC-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
APPLICATION NUMBER: FR 95/02236
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
TELEPHONE: 703-413-3000
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-39

Query Match 100.0%; Score 93; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 4,56-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSNMGCKGRLVCYTS 16
Db 19 LLSNMGCKGRLVCYTS 34

RESULT 4
US-08-894-699-66
Sequence 68, Application US/08894699

Patent No. 6030769

GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENIOR
APPLICANT: LOUSSERT-ARANA, IBITISSAM
APPLICANT: LY, THOI-DIUNG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUBSTADT,
P.C.
STREET: 1753 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC COMPATIBLE
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894, 699
FILING DATE: 01-DEC-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
APPLICATION NUMBER: FR 95/02236
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
TELEPHONE: 703-413-3000
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-66

Query Match 100.0%; Score 93; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 4,56-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSNMGCKGRLVCYTS 16
Db 19 LLSNMGCKGRLVCYTS 34

RESULT 5
US-09-433-4280-30
Sequence 30, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
APPLICANT: Zhang, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
VIRUSES
NUMBER OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1753 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC COMPATIBLE
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/433, 428D
FILING DATE: 01-DEC-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
APPLICATION NUMBER: FR 95/02236
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
TELEPHONE: 703-413-3000
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-66

Query Match 100.0%; Score 93; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 4,56-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSNMGCKGRLVCYTS 16
Db 19 LLSNMGCKGRLVCYTS 34

RESULT 5
US-09-433-4280-30
Sequence 30, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
APPLICANT: Zhang, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
VIRUSES
NUMBER OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1753 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC COMPATIBLE
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/433, 428D
FILING DATE: 01-DEC-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
APPLICATION NUMBER: FR 95/02236
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
TELEPHONE: 703-413-3000
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-66

SEQ ID NO 30
LENGTH: 33
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-4280-30

Query Match 97.8%; Score 91; DB 3; Length 33;
Best Local Similarity 93.8%; Pred. No. 7 6e-08;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 14 LNSMCKGRILVCYTS 29

RESULT 6
US-08-894-699-36
Sequence 36, Application US/08894699
Patent No. 6030769

GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
INVENTOR: SANCOSKI, SEXTON
APPLICANT: SANCOSKI, SEXTON
APPLICANT: LY, THOI-THON
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP C HIV-1, FRAGMENTS OF SUCH
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESS: 1175 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET, FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
COMPUTER FILE: PCOPY.DSK
COMPUTER NAME: C:\COPY\BLS
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patentia Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/894,699
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
PRIORITY NUMBER: PCT/FR96/00294
FILING DATE: 27-FEB-1996
PRIOR APPLICATION NUMBER: FR 95/02336
APPLICATION NUMBER: FR 95/02336
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
PRACTICE ADDRESS NUMBER: 0354-0020-OPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
STRANDS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-36

Query Match 97.8%; Score 91; DB 3; Length 40;
Best Local Similarity 93.8%; Pred. No. 9 2e-08;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNSMCKGRILVCYTS 16
DB 19 LNSMCKGRILVCYTS 34

RESULT 7
US-09-433-4280-4
Sequence 4, Application US/094334280
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: DE LEYS, ROBERT J.
INVENTOR: DE LEYS, ROBERT J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentia Ver. 2.0
SEQ ID NO 33
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-4280-4

Query Match 93.5%; Score 87; DB 3; Length 33;
Best Local Similarity 93.8%; Pred. No. 3 1e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSMCKGRILVCYTS 16
DB 14 LNSMCKGRILVCYTS 29

RESULT 8
US-09-433-4280-7
Sequence 7, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: DE LEYS, ROBERT J.
INVENTOR: ZHENG, JIAN
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentia Ver. 2.0
SEQ ID NO 7
LENGTH: 33
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-4280-7

Query Match 93.5%; Score 87; DB 3; Length 33;
Best Local Similarity 93.8%; Pred. No. 3 1e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSMCKGRILVCYTS 16
DB 14 LNSMCKGRILVCYTS 29

RESULT 9

US-09-433-4280-15
Sequence 15, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: DE LEYS, ROBERT J.
INVENTOR: ZHENG, JIAN
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207


```

RESULT 12
US-09-433-428D-59
; Sequence 59, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 59
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
; OTHER INFORMATION: Sequence
; 09-433-428D-59

```

```

Query Match          92.5%; Score 86; DB 3; Length 23;
Best Local Similarity 86.7%; Pred. No. 3,1e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 LNSMCKGRIVCYTS 16
   |||||:::||||
DB 5 LNSMCKGRIVCYTS 19

```

```

RESULT 13
US-09-433-428D-60
; Sequence 60, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 60
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Xaa is any amino acid
; LOCATION: 1
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
; OTHER INFORMATION: Sequence
; 09-433-428D-60

```

```

Query Match          92.5%; Score 86; DB 3; Length 23;
Best Local Similarity 86.7%; Pred. No. 3,1e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 LNSMCKGRIVCYTS 16
   |||||:::||||
DB 5 LNSMCKGRIVCYTS 19

```

```

RESULT 14
US-09-433-428D-61
; Sequence 61, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian

```

```

; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 61
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
; OTHER INFORMATION: Sequence
; 09-433-428D-61

```

```

Query Match          92.5%; Score 86; DB 3; Length 23;
Best Local Similarity 86.7%; Pred. No. 3,1e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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```

QY 2 LNSMCKGRIVCYTS 16
   |||||:::||||
DB 5 LNSMCKGRIVCYTS 19

```

```

RESULT 15
US-09-433-428D-62
; Sequence 62, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 62
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Xaa is any amino acid
; LOCATION: 6
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
; OTHER INFORMATION: Sequence
; 09-433-428D-62

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```

Query Match          92.5%; Score 86; DB 3; Length 28;
Best Local Similarity 86.7%; Pred. No. 3,8e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 LNSMCKGRIVCYTS 16
   |||||:::||||
DB 10 LNSMCKGRIVCYTS 24

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Search completed: March 22, 2001, 09:52:43
J00 time: 121 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:50:42 ; Search time 65.29 seconds

1.380 Million cells/updates/sec

Title: US-09-147-362-10

Sequence: 1 LMSCKGRLCYTS 16

Scoring table: BLOSUM62

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Searched: 268485 seqs, 34193795 residues

Actual number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Displaying first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	93	100.0	22	19	W80472
3	93	100.0	20	19	W80474
4	93	100.0	20	19	W80476
5	91	100.0	40	17	W07352
6	91	97.8	40	17	W07343
7	90	96.8	32	19	W80469
8	89	95.7	17	19	W80474
9	88	94.6	16	19	W80467
10	88	94.6	22	19	W80461
11	86	93.5	22	19	W80462
12	87	93.5	22	19	W80463

13	87	93.5	23	20	Y05623
14	87	93.5	24	20	Y05624
15	87	93.5	24	20	Y05612
16	87	93.5	42	17	W07353
17	87	93.5	42	17	W07350
18	87	93.5	116	20	Y05555
19	87	93.5	116	20	Y05555
20	87	93.5	715	20	Y05828
21	87	93.5	715	20	Y05828
22	86	92.5	23	20	Y05619
23	86	92.5	41	17	W07351
24	86	92.5	113	20	Y05559
25	86	92.5	113	20	Y05559
26	86	92.5	113	20	Y05557
27	86	92.5	200	21	Y07373
28	86	92.5	215	20	Y09499
29	86	92.5	215	20	Y09499
30	86	92.5	215	20	Y09499
31	86	92.5	245	20	Y09499
32	86	92.5	245	20	Y09499
33	86	92.5	245	21	Y07369
34	86	92.5	281	20	Y09507
35	86	92.5	373	20	Y09495
36	86	92.5	373	20	Y09495
37	86	92.5	460	20	Y09500
38	86	92.5	460	20	Y09500
39	86	92.5	460	20	Y09500
40	86	92.5	460	20	Y09500
41	86	92.5	460	20	Y09500
42	86	92.5	460	20	Y09500
43	86	92.5	490	20	Y09494
44	86	92.5	490	20	Y09494
45	86	92.5	526	20	Y09505

ALIGNMENTS

RESULT 1	
ID	W80468
W80468	standard; peptide: 16 AA.
AC	W80468:
DR	28-JAN-1999 (first entry)
DE	Peptide derived from a conserved sequence of group O human HIV.
DT	Group O human immune deficiency virus; HIV; detection: infection.
OS	Synthetic.
XX	Immune deficiency virus.
XX	W09845323-AL
XX	15-OCT-1998.
XX	06-APR-1998: 98MO-FR00691.
XX	24-FEB-1998: 98FR-0002212.
XX	09-APR-1997: 97FR-0004356.
XX	(SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
XX	Cheneboux DMH, Delagrègne JFH, Gabelle SIX, Rieunier FV.
XX	WPI: 1998-583190/49.
XX	New synthetic peptides - useful for, e.g. detecting infection by
XX	human immune deficiency virus of group O
XX	Claim 6: Page 43; 55pp: French.

CC W80459-74 represent synthetic peptides (either linear or cyclized by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

SO Sequence 16 AA:

Query Match 100.0%; Score 93; DB 19; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.7e-08; Mismatches 0; Gaps 0;

Matches 16; Conservative 0; Indels 0; Gaps 0;

DB 1 LINSWCKGRIVCYTS 16

1 LINSWCKGRIVCYTS 16

UL7 2

W80472 standard; peptide: 22 AA.

W80472:

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

W09845323-A1.

15-OCT-1998.

06-APR-1998: 98MO-FR00691.

24-FEB-1998: 98FR-0002212.

09-APR-1997: 97FR-0004356.

(SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneboux DMB, Delagneau JFH, Godelle SIX, Rieunier FY;

WPI: 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by

human immune deficiency virus of group O

Claim 6; Page 44; 55pp; French.

W80459-74 represent synthetic peptides (either linear or cyclized by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

SO Sequence 22 AA:

Query Match 100.0%; Score 93; DB 19; Length 22;

Best Local Similarity 100.0%; Pred. No. 1e-07; Mismatches 0; Gaps 0;

Matches 16; Conservative 0; Indels 0; Gaps 0;

DB 1 LINSWCKGRIVCYTS 16

1 LINSWCKGRIVCYTS 16

6 LINSWCKGRIVCYTS 21

RESULT 3

W80472 standard; peptide: 28 AA.

W80473:

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

W09845323-A1.

15-OCT-1998.

06-APR-1998: 98MO-FR00691.

24-FEB-1998: 98FR-0002212.

09-APR-1997: 97FR-0004356.

(SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneboux DMB, Delagneau JFH, Godelle SIX, Rieunier FY;

WPI: 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by

human immune deficiency virus of group O

Claim 6; Page 44; 55pp; French.

W80459-74 represent synthetic peptides (either linear or cyclized by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

SO Sequence 28 AA:

Query Match 100.0%; Score 93; DB 19; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.3e-07; Mismatches 0; Gaps 0;

Matches 16; Conservative 0; Indels 0; Gaps 0;

DB 1 LINSWCKGRIVCYTS 16

12 LINSWCKGRIVCYTS 27

RESULT 4

W07346 standard; peptide: 40 AA.

W07346:

03-JUN-1997 (first entry)

Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).

Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O; CVA3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop; primer; hybridisation; amplification; PCR; polymerase chain reaction; immunogen; antibody.

Human immunodeficiency virus type 1.

W09627013-A1.

PT New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 PT antibodies - useful for diagnosis, screening and typing, or as
 PT immunogens

XX Claim 12: Page 33: 71pp: French.

XX Human immunodeficiency virus type 1 (HIV-1) strains are currently divided
 CC into 2 major groups based on the nucleotide sequences of the envelope gene
 CC at the CCR5 and CCR2 coding regions. Group O, and group O containing the
 CC strains AN70 and WPI5180. The invention relates to the discovery of
 CC several new strains of HIV-1 which can be placed in group O, based on the
 CC partial sequences of the CCR5-env, gp1 and gag genes (see R4590/3-OMK
 CC M07329-64). The novel strains have been deposited with the American
 CC 1-1544 (BCF02) (BSS1) 1543 (BCF03) (MAN1) 1542 (BCF04) (MAN2) 1547 (BCF08
 CC (RKO) and 1548 (BCF09) (RKO). The sequence presented here is from the
 CC CCR5 region and corresponds to a fragment of the gp1 protein
 CC encoded by the env gene. The nucleic acids can be used to detect gp- O
 CC HIV-1 strains by hybridisation or (as primers) by gene amplification.
 CC also for screening and typing of such strains. Peptides encoded by the
 CC nucleic acids can be used as immunogens to raise Ab for detecting gp- O
 CC HIV-1.

SQ Sequence 40 AA:

Query Match 97.8%; Score 91; DB 17; Length 40;

Best Local Similarity 93.8%; Pred. No. 3.7e-07; Mismatches 0; Gaps 0;

Matches 15; Conservative 1; Indels 0;

QY 1 LNSMCKGRALVCTTS 16

DB 15 LNSMCKGRALVCTTS 34

RESULT 7

W80469 ID W80469 standard: peptide: 32 AA.

XX W80469:

XX 28-JAN-1999 (first entry)

XX Peptide derived from a conserved sequence of group O human HIV.

XX Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus: HIV; detection: infection.

XX Synthetic.

XX Immune deficiency virus.

XX W09845323-A1.

XX 15-OCT-1998.

XX 06-APR-1998: 98MO-FR00691.

XX 24-FEB-1998: 98FR-0002212.

XX 09-APR-1997: 97FR-0004356.

XX (SNFI) PASTEUR SANOFT DIAGNOSTICS SA.

XX Cheneboux DMB, Delagrange JFH, Gabelle SJX, Rieunier FY;

XX WPI: 1998-583190/49.

XX New synthetic peptide(s) - useful for, e.g. detecting infection by

XX human immune deficiency virus of group O

XX Claim 6: Page 44: 55pp: French.

XX W80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are

CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).

XX Sequence 32 AA:

Query Match 96.8%; Score 90; DB 19; Length 32;

Best Local Similarity 93.8%; Pred. No. 4.2e-07; Mismatches 0; Gaps 0;

Matches 15; Conservative 1; Indels 0;

QY 1 LNSMCKGRALVCTTS 16

DB 11 LNSMCKGRALVCTTS 26

RESULT 8

W80474 ID W80474 standard: peptide: 17 AA.

XX W80474:

XX 28-JAN-1999 (first entry)

XX Peptide derived from a conserved sequence of group O human HIV.

XX Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus: HIV; detection: infection.

XX Synthetic.

XX Immune deficiency virus.

XX W09845323-A1.

XX 15-OCT-1998.

XX 06-APR-1998: 98MO-FR00691.

XX 24-FEB-1998: 98FR-0002212.

XX 09-APR-1997: 97FR-0004356.

XX (SNFI) PASTEUR SANOFT DIAGNOSTICS SA.

XX Cheneboux DMB, Delagrange JFH, Gabelle SJX, Rieunier FY;

XX WPI: 1998-583190/49.

XX New synthetic peptide(s) - useful for, e.g. detecting infection by

XX human immune deficiency virus of group O

XX Claim 6: Page 45: 55pp: French.

XX W80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).

XX Sequence 17 AA:

Query Match 95.7%; Score 89; DB 19; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.2e-07; Mismatches 0; Gaps 0;

Matches 15; Conservative 0; Indels 0;

QY 2 LNSMCKGRALVCTTS 16

DB 2 LNSMCKGRALVCTTS 16

RESULT 9

W80467 ID W80467 standard: peptide: 16 AA.

XX W80467:

XX 28-JAN-1999 (first entry)

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AC W80467:
XX
XX 28-JAN-1999 (first entry)
XX Peptide derived from a conserved sequence of group O human HIV.
XX
XX Group O human immune deficiency virus; HIV; detection; infection.
XX
XX Synthetic.
XX OS Immune deficiency virus.
XX
XX W80845323-A1.
XX
XX 15-OCT-1998.
XX
XX 06-APR-1998; 98MO-FR00691.
XX
XX 24-FEB-1998; 98FR-0002212.
XX
XX 09-APR-1997; 97FR-0004356.
XX
XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.
XX
XX Cheneboux DMB, Delagneau JFH, Gadelle SJX, Rleunier FY;
XX
XX WPI; 1998-583190/49.
XX
XX New synthetic peptide(s) - useful for, e.g. detecting infection by
XX human immune deficiency virus of group O
XX
XX Claim 6; Page 43; 55pp; French.
XX
XX W80459-74 represent synthetic peptides (either linear or cyclised by
XX Cys-Cys disulphide bonds). The peptides represent variable sequences
XX connected around short highly conserved sequences present in isolates
XX of group O human immune deficiency virus (HIV). The peptides are
XX useful as immunological reagents for detecting infection by group O
XX human immune deficiency virus (HIV).
XX
XX Sequence 16 AA:

Query Match
Best Local Similarity 94.6%; Score 88; DB 19; Length 16;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LINSWGCKGRIVCYTS 16
DB 1 LINSWGCKGRIVCYTS 16
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RESULT 10
W80461
W80461
XX W80461 standard; peptide; 22 AA.
XX
XX W80461:
XX
XX 28-JAN-1999 (first entry)
XX
XX Peptide derived from a conserved sequence of group O human HIV.
XX
XX Group O human immune deficiency virus; HIV; detection; infection.
XX
XX Synthetic.
XX OS Immune deficiency virus.
XX
XX W80845323-A1.
XX
XX 15-OCT-1998.
XX
XX 06-APR-1998; 98MO-FR00691.
XX
XX 24-FEB-1998; 98FR-0002212.
XX
XX 09-APR-1997; 97FR-0004356.
XX

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XX
XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.
XX
XX Cheneboux DMB, Delagneau JFH, Gadelle SJX, Rleunier FY;
XX
XX WPI; 1998-583190/49.
XX
XX New synthetic peptide(s) - useful for, e.g. detecting infection by
XX human immune deficiency virus of group O
XX
XX Claim 6; Page 42; 55pp; French.
XX
XX W80459-74 represent synthetic peptides (either linear or cyclised by
XX Cys-Cys disulphide bonds). The peptides represent variable sequences
XX connected around short highly conserved sequences present in isolates
XX of group O human immune deficiency virus (HIV). The peptides are
XX useful as immunological reagents for detecting infection by group O
XX human immune deficiency virus (HIV).
XX
XX Sequence 22 AA:

Query Match
Best Local Similarity 94.6%; Score 88; DB 19; Length 22;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LINSWGCKGRIVCYTS 16
DB 1 LINSWGCKGRIVCYTS 16
||:|||||||||||||||

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RESULT 11
W80462
W80462
XX W80462 standard; peptide; 22 AA.
XX
XX W80462:
XX
XX 28-JAN-1999 (first entry)
XX
XX Peptide derived from a conserved sequence of group O human HIV.
XX
XX Group O human immune deficiency virus; HIV; detection; infection.
XX
XX Synthetic.
XX OS Immune deficiency virus.
XX
XX W80845323-A1.
XX
XX 15-OCT-1998.
XX
XX 06-APR-1998; 98MO-FR00691.
XX
XX 24-FEB-1998; 98FR-0002212.
XX
XX 09-APR-1997; 97FR-0004356.
XX
XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.
XX
XX Cheneboux DMB, Delagneau JFH, Gadelle SJX, Rleunier FY;
XX
XX WPI; 1998-583190/49.
XX
XX New synthetic peptide(s) - useful for, e.g. detecting infection by
XX human immune deficiency virus of group O
XX
XX Claim 6; Page 42; 55pp; French.
XX
XX W80459-74 represent synthetic peptides (either linear or cyclised by
XX Cys-Cys disulphide bonds). The peptides represent variable sequences
XX connected around short highly conserved sequences present in isolates
XX of group O human immune deficiency virus (HIV). The peptides are
XX useful as immunological reagents for detecting infection by group O
XX human immune deficiency virus (HIV).
XX

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XX	PF	20-JUL-1998:	98MO-EF04522.
XX	XX		
XX	XR	18-JUL-1997:	97EP-0870110.
XX	XW		
XX	PA	(INNO-) INNOGENETICS NV.	
XX	PI	Delaporte E., Peeters M., Saman E., Vanden Haesevelde M,	
XX	DR	WPI: 1999-132255/J11.	
XX	PT	New isolated HIV-1 group O strains - used to produce	
XX	PR	polyclonal antisera, antigens and antibodies for use in diagnosis and in	
XX	PP	vaccines for prevention of HIV-1 infection	
XX	PS	Claim 2; Page 90; 162pp; English.	
CC	CC	The present sequence is an antigen of the gp160 env precursor	
CC	CC	protein of HIV-1 group O (Outlier) strain MP645, an isolate from	
CC	CC	Cameron. The invention relates to new HIV-1 group O antigens (see	
CC	CC	05344-623), and the use of these antigens, or nucleic acids (see	
CC	CC	AIDS). They can be used as reagents for detecting HIV-1 group O	
CC	CC	infection and for diagnostic purposes in different types of HIV-1 group O	
CC	CC	infection. In particular against HIV-1 group O completely against HIV-1	
CC	CC	at least one HIV-1 type O antigen, a nucleic acid encoding such an	
CC	CC	antigen, a virus-like particle comprising such an antigen, or an	
CC	CC	recombinant form of an HIV-1 type O strain. The invention also	
CC	CC	relates to new HIV-1 group O strains, mostly from patients from	
CC	CC	Cameron and its neighbouring countries.	
SO	Sequence	24 AA;	
	Query Match:	93.5%; Score 87; DB 20; Length 24;	
	Local Similarity	93.8%; Pred. No. 8,9e-07;	
	Matches 15; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
OY	1 LUNSGCKGRATCTG 16		
DB	4 LLHWGKGRIVCYGA 19		
RESULT 15			
Y05612	ID	Y05612 standard; Peptide: 24 AA.	
Y05612:			
DT	19-JUL-1999	(first entry)	
XX	DM	HIV-1 group O strain 772P94 gp160 env precursor protein antigen.	
XX	DW	HIV-1 group O; Outlier strain; v3 hypervariable region; gp160;	
XX	KM	envelope protein; antigen; vaccine; diagnosis; AIDS.	
XX	OS	Human immunodeficiency virus type 1.	
XX	XX	MO9094011-A2.	
XX	XX		
XX	PD	28-JAN-1999.	
XX	PF	20-JUL-1998: 98MO-EF04522.	
XX	PR	18-JUL-1997: 97EP-0870110.	
XX	XX	(INNO-) INNOGENETICS NV.	
XX	PI	Delaporte E., Peeters M., Saman E., Vanden Haesevelde M,	
XX	DR	WPI: 1999-132255/J11.	
XX	PT	New isolated HIV-1 group O strains - used to produce	
XX	PR	polyclonal antisera, antigens and antibodies for use in diagnosis and in	
XX	PP	vaccines for prevention of HIV-1 infection	
XX	PS	Claim 2; Page 90; 162pp; English.	
CC	CC	The present sequence is an antigen of the gp160 env precursor	
CC	CC	protein of HIV-1 group O (Outlier) strain MP645, an isolate from	
CC	CC	Cameron. The invention relates to new HIV-1 group O antigens (see	
CC	CC	05344-623), and the use of these antigens, or nucleic acids (see	
CC	CC	AIDS). They can be used as reagents for detecting HIV-1 group O	
CC	CC	infection and for diagnostic purposes in different types of HIV-1 group O	
CC	CC	infection. In particular against HIV-1 group O completely against HIV-1	
CC	CC	at least one HIV-1 type O antigen, a nucleic acid encoding such an	
CC	CC	antigen, a virus-like particle comprising such an antigen, or an	
CC	CC	recombinant form of an HIV-1 type O strain. The invention also	
CC	CC	relates to new HIV-1 group O strains, mostly from patients from	
CC	CC	Cameron and its neighbouring countries.	
SO	Sequence	24 AA;	

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P1 New isolated HIV-1 group O strains - used to produce
P2 polynucleotides, antigens and antibodies for use in diagnosis and in
P3 vaccines for prevention of HIV-1 infection
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P832
P833

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Search completed: March 22, 2001, 09:51:53
Job time: 71 sec

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Query Match          99.5%: Score 87:  Db 20: Length 24:
Best Local Similarity 99.8%:
Matches 15: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
QY      1  LINSNGCGKRIACVYS 16
        |||L|||||
Db       4  LINSNGKRIACVYS 19

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Fri Mar 23 07:47:19 2001

us-09-147-362-10.rag

Page 8

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using SW model

Run on: March 22, 2001, 09:52:43 ; Search time 46.96 Seconds
(without alignments)
12,236 Million cell updates/sec

Title: US-09-147-362-11

Perfect score: 176

Sequence: 1 ALPTLLNQQLINSMGRCGRVCYSYVNNET 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

tal number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2.6/p1cdat2/2/1aa/5A.COMB.pep.*
- 2: /cgn2.6/p1cdat2/2/1aa/5B.COMB.pep.*
- 3: /cgn2.6/p1cdat2/2/1aa/6.COMB.pep.*
- 4: /cgn2.6/p1cdat2/2/1aa/PCFUS.COMB.pep.*
- 5: /cgn2.6/p1cdat2/2/1aa/backfill1.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	163	97.5	215	2	US-08-894-699-39	Sequence 39, Appl
2	161	97.5	215	2	US-08-912-129A-58	Sequence 48, Appl
3	161	91.5	245	2	US-08-912-129A-52	Sequence 48, Appl
4	161	91.5	373	2	US-08-912-129A-52	Sequence 52, Appl
5	161	91.5	460	2	US-08-912-129A-50	Sequence 60, Appl
6	161	91.5	480	2	US-08-912-129A-50	Sequence 60, Appl
7	161	91.5	618	2	US-08-912-129A-54	Sequence 54, Appl
8	161	91.5	873	2	US-08-912-129A-51	Sequence 51, Appl
9	158	89.8	333	3	US-08-894-699-67	Sequence 67, Appl
10	158	89.8	333	3	US-08-894-699-67	Sequence 67, Appl
11	158	89.8	403	3	US-08-894-699-68	Sequence 68, Appl
12	158	89.8	356	1	US-08-602-713-12	Sequence 12, Appl
13	158	89.8	356	3	US-08-989-493-12	Sequence 12, Appl
14	157	89.2	413	3	US-08-894-699-69	Sequence 69, Appl
15	156	88.6	413	3	US-08-433-428D-6	Sequence 6, Appl
16	156	88.6	413	3	US-08-433-428D-30	Sequence 30, Appl
17	156	88.6	413	3	US-08-894-699-67	Sequence 67, Appl
18	156	88.6	413	3	US-08-894-699-67	Sequence 67, Appl
19	156	88.6	413	3	US-08-894-699-67	Sequence 67, Appl
20	155	86.9	403	3	US-08-894-699-40	Sequence 40, Appl
21	155	86.9	403	3	US-08-433-428D-10	Sequence 10, Appl
22	155	86.9	403	3	US-08-433-428D-4	Sequence 4, Appl
23	152	86.4	333	3	US-09-433-428D-7	Sequence 7, Appl
24	152	86.4	333	3	US-09-433-428D-15	Sequence 15, Appl
25	152	86.4	423	3	US-08-894-699-66	Sequence 66, Appl
26	151	85.8	333	3	US-09-433-428D-5	Sequence 5, Appl
27	151	85.8	333	3	US-09-433-428D-5	Sequence 5, Appl
28	150	85.2	333	3	US-09-433-428D-8	Sequence 8, Appl

29	149	84.7	33	3	US-09-433-428D-15	Sequence 15, Appl
30	149	84.7	33	3	US-09-433-428D-21	Sequence 21, Appl
31	149	84.7	33	3	US-09-433-428D-27	Sequence 27, Appl
32	147	83.5	33	3	US-09-433-428D-9	Sequence 9, Appl
33	147	83.5	33	3	US-09-433-428D-14	Sequence 14, Appl
34	147	83.5	33	3	US-09-433-428D-26	Sequence 26, Appl
35	147	83.5	33	3	US-09-433-428D-29	Sequence 29, Appl
36	147	83.5	403	3	US-08-894-699-41	Sequence 41, Appl
37	146	83.0	333	3	US-09-433-428D-11	Sequence 11, Appl
38	145	82.4	333	3	US-09-433-428D-18	Sequence 18, Appl
39	145	82.4	333	3	US-09-433-428D-18	Sequence 18, Appl
40	145	82.4	333	3	US-09-433-428D-18	Sequence 18, Appl
41	144	81.8	333	3	US-09-433-428D-28	Sequence 28, Appl
42	143	81.2	149	3	US-09-433-428D-67	Sequence 67, Appl
43	143	81.2	220	3	US-09-433-428D-65	Sequence 65, Appl
44	143	81.2	368	3	US-09-433-428D-58	Sequence 58, Appl
45	143	81.2	439	3	US-09-433-428D-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-08-894-699-39
Sequence 39, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIRON, FRANCIS
APPLICANT: SIRON, FRANCIS
APPLICANT: SIRON, FRANCIS
APPLICANT: LOUSSEPT-ALAKA, IBTISSEM
APPLICANT: LY, THOI-DUONG, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESS: SIRON, SPYKAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.O.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET, FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894, 699
FILING DATE: 01-DEC-1997
CLASSIFICATION: DNTA:
PRIORITY INFORMATION:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: ORLON, NORMAN F., 614
REGISTRATION NUMBER: 01354-0020-01CCT
TELEPHONE: 703-413-3000
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-413-2220
INFORMATION FOR SPO ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDNESS: single
MOLECULE TYPE: peptide

US-08-894-699-39

Query Match 95.5%; Score 161; DB 3; Length 40;

Best Local Similarity 90.6%; Pred. No. 5, 1e-18;

Matches 27; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 9 ALETLIONQOLLNSMCKGRIVCYTSVKNMET 40

RESULT 2

US-08-912-129A-58

Sequence 58; Application US/08912129A

Patent No. 5922533

GENERAL INFORMATION:

APPLICANT: VALLARI, ANADRUZELA S.

APPLICANT: HACKETT, JOHN JR.

APPLICANT: HICKMAN, ROBERT K.

APPLICANT: VARTER, VINCENT A. JR.

APPLICANT: NECKLAMS, ELIZABETH A.

APPLICANT: GODDEN, ALAN M. JR.

APPLICANT: BRENNAN, CATHERINE A.

APPLICANT: DEVARE, SUSHIL G.

TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:

ADDRESS: Abbott Laboratories

STREET: 100 Abbott Park Road

STATE: Abbott Park

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.44 MB

OPERATING SYSTEM: MS-DOS (Windows 95)

SOFTWARE: Microsoft Word (ASCII format output)

CUSTOMER APPLICATION DATA:

FILING DATE: 15-AUG-1997

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

REGISTERED ADDRESS: M. J. 652

REFERENCE/DOCKET NUMBER: 6109.US.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-937-9803

TELEFAX: 847-938-2623

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

US-08-912-129A-58

Query Match 91.5%; Score 161; DB 2; Length 215;

Best Local Similarity 84.4%; Pred. No. 3, 6e-16;

Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

DB 117 ALETLIONQOLLNSMCKGRIVCYTSVKNMET 32

RESULT 3

US-08-912-129A-48

Sequence 48; Application US/08912129A

Patent No. 5922533

GENERAL INFORMATION:

APPLICANT: VALLARI, ANADRUZELA S.

APPLICANT: HACKETT, JOHN JR.

APPLICANT: HICKMAN, ROBERT K.

APPLICANT: VARTER, VINCENT A. JR.

APPLICANT: NECKLAMS, ELIZABETH A.

APPLICANT: GODDEN, ALAN M. JR.

APPLICANT: BRENNAN, CATHERINE A.

APPLICANT: DEVARE, SUSHIL G.

TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:

ADDRESS: Abbott Laboratories

STREET: 100 Abbott Park Road

STATE: Abbott Park

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.44 MB

OPERATING SYSTEM: MS-DOS (Windows 95)

SOFTWARE: Microsoft Word (ASCII format output)

CUSTOMER APPLICATION DATA:

FILING DATE: 15-AUG-1997

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

REGISTERED ADDRESS: M. J. 652

REFERENCE/DOCKET NUMBER: 6109.US.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-937-9803

TELEFAX: 847-938-2623

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 amino acids

TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-912-129A-48

Query Match 91.5%; Score 161; DB 2; Length 245;

Best Local Similarity 84.4%; Pred. No. 3, 1e-16;

Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

DB 117 ALETLIONQOLLNSMCKGRIVCYTSVKNMET 32

RESULT 4

US-08-912-129A-52

Sequence 52; Application US/08912129A

Patent No. 5922533

GENERAL INFORMATION:

APPLICANT: VALLARI, ANADRUZELA S.

APPLICANT: HACKETT, JOHN JR.

APPLICANT: HICKMAN, ROBERT K.

APPLICANT: VARTER, VINCENT A. JR.

APPLICANT: NECKLAMS, ELIZABETH A.

APPLICANT: GODDEN, ALAN M. JR.

APPLICANT: BRENNAN, CATHERINE A.

APPLICANT: DEVARE, SUSHIL G.

```

? TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
? NUMBER OF SEQUENCES: 89
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Abbott Laboratories
? STREET: 100 Abbott Park Road
? CITY: Abbott Park
? STATE: IL
? COUNTRY: USA
? ZIP: 60064-3500
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
? OPERATING SYSTEM: IBM Compatible
? SOFTWARE: Microsoft Word (Windows 95)
? CURRENT APPLICATION DATA: (ASCII format output)
? FILING DATE: 15-AUG-1997
? CLASSIFICATION: 436
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Danckwerts, Andreas M.
? REGISTRATION NUMBER: 32,652
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 847-937-9803
? TELEFAX: 847-938-2623
? TELEX:
? INFORMATION FOR SEQ ID NO: 52:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 373 amino acids
? STRANDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-912-129A-52

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Query Match          91.5%; Score 161; DB 2; Length 373;
Best Local Similarity 84.4%; Pred. No. 6,7e-16;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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? 1 ALETLI000LINSWGRGRVCYSVANNET 32
? |||||:|||||:|||||:|||||:|||||
? DB 117 ALETLI000LINSWGRGRVCYSVANNET 148

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? SOUT 5
? US-08-912-129A-60
? Sequence 60; Application US/08912129A
? Patent No. 592533
? GENERAL INFORMATION:
? APPLICANT: VALLARI, ANDRUEZELA S.
? APPLICANT: HACKETT, JOHN JR.
? APPLICANT: HICKMAN, ROBERT K.
? APPLICANT: VARITER, VINCENT A. JR.
? APPLICANT: NECKLAMS, ELIZABETH A.
? APPLICANT: GOLDEN, ALAN M.
? APPLICANT: BRENNAN, CATHERINE A.
? APPLICANT: DEYARE, SUSHIL G.
? TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
? NUMBER OF SEQUENCES: 89
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Abbott Laboratories
? STREET: 100 Abbott Park Road
? CITY: Abbott Park
? STATE: IL
? COUNTRY: USA
? ZIP: 60064-3500
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
? COMPUTER: IBM Compatible

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? OPERATING SYSTEM: MS-DOS (Windows 95)
? SOFTWARE: Microsoft Word (ASCII format output)
? CURRENT APPLICATION DATA: (ASCII format output)
? APPLICATION NUMBER: US/08/912,129A
? FILING DATE: 15-AUG-1997
? CLASSIFICATION: 436
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Danckwerts, Andreas M.
? REGISTRATION NUMBER: 32,652
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 847-937-9803
? TELEFAX: 847-938-2623
? TELEX:
? INFORMATION FOR SEQ ID NO: 60:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 460 amino acids
? STRANDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: Protein
? US-08-912-129A-60

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Query Match          91.5%; Score 161; DB 2; Length 460;
Best Local Similarity 84.4%; Pred. No. 6,4e-16;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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? 1 ALETLI000LINSWGRGRVCYSVANNET 32
? |||||:|||||:|||||:|||||:|||||
? DB 362 ALETLI000LINSWGRGRVCYSVANNET 933

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? RESUIT 5
? US-08-912-129A-50
? Sequence 50; Application US/08912129A
? Patent No. 592533
? GENERAL INFORMATION:
? APPLICANT: VALLARI, ANDRUEZELA S.
? APPLICANT: HACKETT, JOHN JR.
? APPLICANT: HICKMAN, ROBERT K.
? APPLICANT: VARITER, VINCENT A. JR.
? APPLICANT: NECKLAMS, ELIZABETH A.
? APPLICANT: GOLDEN, ALAN M.
? APPLICANT: BRENNAN, CATHERINE A.
? APPLICANT: DEYARE, SUSHIL G.
? TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
? NUMBER OF SEQUENCES: 89
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Abbott Laboratories
? STREET: 100 Abbott Park Road
? CITY: Abbott Park
? STATE: IL
? COUNTRY: USA
? ZIP: 60064-3500
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
? OPERATING SYSTEM: IBM Compatible
? SOFTWARE: Microsoft Word (Windows 95)
? CURRENT APPLICATION DATA: (ASCII format output)
? APPLICATION NUMBER: US/08/912,129A
? FILING DATE: 15-AUG-1997
? CLASSIFICATION: 436
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Danckwerts, Andreas M.
? REGISTRATION NUMBER: 32,652

```

REFERENCE/DOCKET NUMBER: 6109 US:01
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-50

Query Match 91.5%: Score 161; DB 2; Length 490;
Best Local Similarity 84.4%: Pred. No. 9.1e-15;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 ALETLNQNOLNMGCKRGILCTYSVMNET 32
362 ALETLNQNOLNMGCKRGILCTYSVMNET 393

RESULT 7
US-08-912-129A-54
Sequence 54 Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITER, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVRAN, SUSHLI G.
APPLICANT: INVERDIE, JENNIFER
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
ZIP: 60064-3500
COUNTRY: USA
COMPUTER: IBM compatible
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA: US/08/912/129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M.
REGISTRATION NUMBER: 32,652
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-912-129A-54

Query Match 91.5%: Score 161; DB 2; Length 618;
Best Local Similarity 84.4%: Pred. No. 1.2e-15;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 ALETLNQNOLNMGCKRGILCTYSVMNET 32
362 ALETLNQNOLNMGCKRGILCTYSVMNET 393

RESULT 8
US-08-912-129A-61
Sequence 61 Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITER, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVRAN, SUSHLI G.
APPLICANT: INVERDIE, JENNIFER
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
ZIP: 60064-3500
COUNTRY: USA
COMPUTER: IBM compatible
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA: US/08/912/129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M.
REGISTRATION NUMBER: 32,652
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 873 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-61

Query Match 91.5%: Score 161; DB 2; Length 873;
Best Local Similarity 84.4%: Pred. No. 1.7e-15;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 ALETLNQNOLNMGCKRGILCTYSVMNET 32
591 ALETLNQNOLNMGCKRGILCTYSVMNET 622

RESULT 9
US-09-433-4280-25
Sequence 25, Application US/09433428D
GENERAL INFORMATION:
APPLICANT: DB 199, Robert J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 25
LENGTH: 33
TYPE: PRT
ORGANISM: Human Immunodeficiency virus type 1
US-09-433-4280-25

Query Match 89.8%; Score 158; DB 3; Length 33;
Best Local Similarity 90.0%; Pred. No. 1,2e-16;
Matches 27; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ALEFLIQNQLNSMCKGRVCTSVNM 30
DB 4 ALEFLIQNQLNSMCKGRVCTSVNM 33

RESULT 10
US-09-433-4280-25
Sequence 25, Application US/08894699
GENERAL INFORMATION:
APPLICANT: SARACOSTI, SIMON, FRANCOIS
APPLICANT: LOUSSEST-ALAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIK-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
STATE: ARLINGTON
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-OPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-36
Query Match 89.8%; Score 158; DB 3; Length 40;
Best Local Similarity 84.4%; Pred. No. 1,5e-16;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ALEFLIQNQLNSMCKGRVCTSVNM 32
DB 9 ALEFLIQNQLNSMCKGRVCTSVNM 40

RESULT 11
US-08-894-699-36
Sequence 68, Application US/08894699
GENERAL INFORMATION:
APPLICANT: SARACOSTI, SIMON, FRANCOIS
APPLICANT: LOUSSEST-ALAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIK-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
STATE: ARLINGTON
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-OPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-36

Query Match 89.8%; Score 158; DB 3; Length 40;
 Best Local Similarity 87.5%; Pred. No. 1.7e-15;
 Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 ALETLQNOQLNSMCKGRGLVCTYSVNNET 32
 |||||.....
 Db 9 ALETLQNOQLNSMCKGRGLVCTYSVNNET 40

RESULT 12
 US-08-602-713-12
 Sequence 12, Application US/08602713
 Patient No. 5728205
 GENERAL INFORMATION:
 APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan;
 APPLICANT: G. Rlier, Lutz G.; Bberle, Josef; Kapue, Lazare;
 APPLICANT: Zekeng, L. Olof Achenqui
 TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use
 TITLE OF INVENTION: (HVP-2901/94)
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESS: 805 Third Avenue
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 Inch, 360 kb storage
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/602,713
 FILING DATE: 16-FEBRUARY-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 195 05 262
 FILING DATE: 16-FEBRUARY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 5798205man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LEDER 203
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 688-9200
 INFORMATION FOR SDO ID NO: 12;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 356 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: Protein
 FRAGMENT TYPE: Internal
 US-08-602-713-12

Query Match 89.8%; Score 158; DB 1; Length 356;
 Best Local Similarity 81.2%; Pred. No. 1.7e-15;
 Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ALETLQNOQLNSMCKGRGLVCTYSVNNET 32
 |||||.....
 Db 312 ALETLQNOQLNSMCKGRGLVCTYSVNNET 343

RESULT 13
 US-08-989-493-12
 Sequence 12, Application US/08989493
 Patient No. 6162631
 GENERAL INFORMATION:
 APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan;
 APPLICANT: G. Rlier, Lutz G.; Bberle, Josef; Kapue, Lazare;

APPLICANT: Zekeng, L. Olof Achenqui
 TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use
 TITLE OF INVENTION: (HVP-2901/94)
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESS: Felfe & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 Inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/989,493
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/602,713
 FILING DATE: 16-FEBRUARY-1996
 APPLICATION NUMBER: DE 195 05 262
 FILING DATE: 16-FEBRUARY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 5798205man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LEDER 203
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 688-9200
 INFORMATION FOR SDO ID NO: 12;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 356 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: Protein
 FRAGMENT TYPE: Internal
 US-08-989-493-12

Query Match 89.8%; Score 158; DB 3; Length 356;
 Best Local Similarity 81.2%; Pred. No. 1.7e-15;
 Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ALETLQNOQLNSMCKGRGLVCTYSVNNET 32
 |||||.....
 Db 312 ALETLQNOQLNSMCKGRGLVCTYSVNNET 343

RESULT 14
 US-08-994-699-69
 Sequence 69, Application US/08994699
 Patient No. 6030769
 GENERAL INFORMATION:
 APPLICANT: SIMON, FRANCOIS
 APPLICANT: SARAGOSTI, SENTOB
 APPLICANT: LOUSSERT-ANNA, IBITISSAM
 APPLICANT: LIT, ROBERT
 APPLICANT: LIT, RANDER MARIE-LAURE
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
 ADDRESSEE: P.C.
 STREET: 1725 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 STREET: 1725
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA

Job time: 121 sec

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: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: PUBLICATION NUMBER: US/08/894,699
: FILING DATE: 01 DEC 1997
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: PCT/FR96/00294
: FILING DATE: 26-FEB-1996
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: FR 95/02236
: FILING DATE: 17-FEB-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: OHLON, NORMAN F.
: REGISTRATION NUMBER: 24,614
: REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-413-3000
: TELEFAX: 703-413-2220
: INFORMATION FOR SEQ ID NO: 69:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 44 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-894-699-69

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Query Match      89.28; Score 157; DB 3; Length 41;
Best Local Similarity 84.48; Freq. No. 2, 3e-16;
Matches 27; Conservative 3; Mismatches 2; Indels 0; Gaps 0:
QY 1 ALETTLQNOOLLNSMCGKRGRLVCYTSVANNMT 32
DB 9 ALETTLQNOOLLNSMCGKRGRLVCYTSVANNMT 40

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RESULT 15
US-09-433-428D-6
: Sequence 6, Application US/09433428D
: Patent No. 6145910
: GENERAL INFORMATION:
: APPLICANT: De Leys, Robert J.
: TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
: PUBLICATION NUMBER: US/09/433,428D
: CURRENT FILING DATE: 1995-11-04
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 6
: TYPE: PRT
: LENGTH: 33
: ORGANSISM: Human immunodeficiency virus type 1
: US-09-433-428D-6

```

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Query Match      88.68; Score 156; DB 3; Length 33;
Best Local Similarity 90.08; Freq. No. 2, 3e-16;
Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0:
QY 1 ALETTLQNOOLLNSMCGKRGRLVCYTSVANN 30
DB 4 ALETTLQNOOLLNSMCGKRGRLVCYTSVANN 33

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Search completed: March 22, 2001, 09:52:43

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: March 22, 2001, 09:51:53 : Search time 65.29 seconds

(without alignment)

File: US-09-147-362-11

Perfect score: 176

Sequence: 1 ALDTLLNQDLNMGCRGRVCYTVRNKNT 32

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1:	/A/Geneseq_36.*
2:	/SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.*
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21:	/SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	100.0	32	19	W80469
2	170	96.6	32	19	W80470
3	168	95.5	40	17	W07346
4	165	93.8	32	19	W80471
5	161	91.5	200	21	Y77373
6	161	91.5	215	20	Y09499
7	161	91.5	215	20	Y09498
8	161	91.5	215	20	Y09493
9	161	91.5	245	21	Y08459
10	161	91.5	245	20	Y08977
11	161	91.5	245	21	Y77369
12	161	91.5	281	20	Y09507

13	161	91.5	373	20	Y09465	HIV-1 group O env
14	161	91.5	372	20	Y08975	Recombinant pCO-11
15	161	91.5	460	20	Y09400	Recombinant pCO-8C
16	161	91.5	460	21	Y09584	HIV-1 group O env
17	161	91.5	460	21	Y77375	HIV-1 group O env
18	161	91.5	474	21	Y77371	HIV-1 group O env
19	161	91.5	488	20	Y09504	HIV-1 group O env
20	161	91.5	490	20	Y09494	Recombinant pCO-9C
21	161	91.5	490	20	Y09578	HIV-1 group O env
22	161	91.5	530	21	Y77370	HIV-1 group O env
23	161	91.5	618	20	Y09496	Recombinant pCO-11
24	161	91.5	618	20	Y09498	HIV-1 group O env
25	161	91.5	618	20	Y09580	HIV-1 group O env
26	161	91.5	618	21	Y77372	HIV-1 group O env
27	161	91.5	706	20	Y09503	HIV-1 group O env
28	161	91.5	736	20	Y09502	HIV-1 group O env
29	161	91.5	873	20	Y09501	HIV-1 group O env
30	161	91.5	873	21	Y77376	Amino acid sequenc
31	161	91.5	873	21	Y77375	HIV-1 group O Isol
32	158	89.8	40	17	W07342	Partial sequence o
33	158	89.8	40	17	W07343	Partial sequence o
34	158	89.8	116	20	Y09555	Partial sequence o
35	158	89.8	356	17	W03940	gp 41 antigen of H
36	157	89.2	41	17	W07353	Partial sequence o
37	157	89.2	113	20	Y09546	HIV-1 group O Isol
38	157	89.2	117	20	Y09548	HIV-1 group O Isol
39	156	88.6	41	17	W07351	Partial sequence o
40	156	88.6	110	20	Y09552	HIV-1 group O Isol
41	156	88.6	710	20	Y09553	HIV-1 group O Isol
42	155	88.1	104	17	W07245	HIV-1 group O Isol
43	155	88.1	110	20	Y09553	HIV-1 group O Isol
44	155	88.1	113	20	Y09551	HIV-1 group O Isol
45	155	88.1	113	20	Y09550	HIV-1 group O Isol

ALIGNMENTS

RESULT 1	ID	W80469	W80469 standard; peptide: 32 AA:
	AC	W80469:	28-JAN-1999 (first entry)
	DC		Peptide derived from a conserved sequence of group O human HIV.
	KW		Group O human immune deficiency virus; HIV; detection; Infection.
	OS		Synthetic.
	XS		Immune deficiency virus.
	XX		W09845323-A1.
	PD		15-OCT-1998.
	XX		
	PF		06-APR-1998: 9880-PR00691.
	XX		
	PR		24-FEB-1998: 988R-0002212.
	XX		
	PR		09-APR-1997: 97FR-0004356.
	XX		
	PI		(SNFI) PASTEREUR SANOFI DIAGNOSTICS SA.
	XX		Cheneboux DMB, Delagrange JH, Gadellet SXH, Rieunier FY;
	DR		WPI: 1998-583190/49.
	XX		
	PP		New synthetic peptide(s) - useful for, e.g. detecting infection by
	PR		human immune deficiency virus of group O
	XX		
	XX		Claim 6: Page 44: 55pp: French.
	XX		

DT 28-JAN-1999 (first entry)
 XX Peptide derived from a conserved sequence of group O human HIV.
 DE Group O human immune deficiency virus; HIV; detection; infection.
 XX Synthetic.
 OS Immune deficiency virus.
 XX MO9845323-AL.
 PN 15-OCT-1998.
 PD 06-APR-1998: 98MO-FR00691.
 XX 24-FEB-1998: 98ER-0002212.
 PR 09-APR-1997: 97ER-0004356.
 XX (SNF) PASTEUR SANOI DIACNOSTICS SA.
 PA Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY.
 DR WPI: 1998-583190/49.
 XX New synthetic peptide(s) - useful for e.g. detecting infection by
 PT human immune deficiency virus of group O
 XX Claim 6; Page 44; 55pp; French.
 PS H80459-74 represent synthetic peptides (either linear or cyclized by
 CC C-terminal amide bonds). The peptides represent variable sequences
 CC connected to conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX Sequence 32 AA:
 SQ
 Query Match 93.8%, Score 165; DB 19; Length 32;
 Best Local Similarity 93.8%; Pred. No. 2, 7e-15;
 Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALETLQNGQLNSMCGRGLVCYSVARNET 32
 DB 1 aletliqngqlnlwgcrglvcysvavnet 32
 SUIT 5
 ID 77373 standard; Protein: 200 AA.
 AC 77373:
 XX 22-MAY-2000 (first entry)
 DE HIV-1 group O env gp120/gp41 pCO-5 recombinant protein, SEQ ID NO:56.
 XX HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;
 KM immunosay; positive control; affinity purification; therapeutic;
 KM Scherichla coli; antigen; synthetic gene construction; mutagen;
 KM deletion mutation.
 XX Human immunodeficiency virus type 1 group O isolate HMI12.
 OS Synthetic.
 XX MO200004383-A2.
 PN 27-JAN-2000.
 PD 09-JUL-1999: 99MO-US15469.
 XX 14-JUL-1998: 98US-0115171.

XX (AB80) ABBOTT LAB.
 PA Scheffell JW, Heckett JR, Tyner JD, Hickman RK.
 XX WPI: 2000-171290/15.
 DR N-PSDB: 290284.
 XX Novel monoclonal antibodies useful as positive control reagent for
 PT detecting human immunodeficiency virus infections and diagnosing,
 PT evaluating or prognosing viral disease -
 XX Example 3; Fig 9; 148pp; English.
 CC The invention relates to anti-HIV-1 group O monoclonal antibodies, which
 CC may be used as positive control reagents in assays to detect and
 CC differentiate HIV-1 infections. The invention also relates to a
 CC monoclonal antibody which binds specifically to an HIV-1 group O antigen,
 CC which has no more than 15% gross reactivity to a corresponding antigen
 CC selected from HIV-1 group M antigens and HIV-2 antigens; and a method of
 CC using a monoclonal antibody as a positive control reagent in an
 CC immunological assay for the detection of anti-HIV-1 group O antibodies. The
 CC monoclonal antibodies are also useful for detecting HIV-1 group O
 CC immunosays involving coupling a monoclonal antibody
 CC antigen and detecting the antigen-antibody complex. The monoclonal
 CC antibodies of the invention would be used to ensure that the reagents
 CC provided to detect HIV-1 group O antibody were performing properly. The
 CC monoclonal antibodies may also can be immobilised on a matrix and used
 CC for the detection of specific HIV-1 group O-derived proteins from
 CC cell cultures or biological samples. The monoclonal antibodies can also
 CC be used for generating chimeric vaccines. The monoclonal antibodies may
 CC synthetic, recombinant or purified antibodies which may be used to
 CC evaluate, or prognosticate HIV disease condition. The monoclonal
 CC antibodies are also useful for differentiating HIV-1 group O antigens
 CC from HIV-1 group M and HIV-2 antigens. Sequences Y7369-Y7375 represent
 CC recombinant HIV-1 group O env proteins encoded by the synthetic genes
 CC 290280-290286. The recombinant HIV-1 env proteins contain various
 CC deletions relative to the recombinant HIV-1 isolate HMI12 isolate
 CC recombinant HIV-1 group O antigens were purified and used to screen
 CC hybridoma cultures.
 XX Sequence 200 AA:
 SQ
 Query Match 91.5%, Score 161; DB 21; Length 200;
 Best Local Similarity 84.4%; Pred. No. 6, 1e-14;
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALETLQNGQLNSMCGRGLVCYSVARNET 32
 DB 102 aletliqngqlnlwgcrglvcysvavnet 133
 RESULT 6
 ID Y09499 standard; Protein: 215 AA.
 AC Y09499:
 XX 15-JUL-1999 (first entry)
 DE HIV-1 group O env polypeptide pCO-8PL.
 XX HIV; human immunodeficiency virus; antigen; detection; antibody;
 KM differentiation; Group O; env; immunogen; immunosay.
 XX Human immunodeficiency virus type 1.
 XX MO9909179-A2.
 PN 25-FEB-1999.

XX 17-AUG-1998; 98MO-US17014.
 PF 15-AUG-1997; 97US-0911824.
 PR (ABBO) ABBOTT LAB.
 XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;
 PI WPI: 1999-190167/16.
 DR N-PSDB: X56078.
 XX New isolated HIV-1 Group O env polypeptides - used for the
 PT detection of anti-HIV antibodies and for the production of
 PT antibodies for use in detection, purification and therapy
 PS Claim 17; Fig 5; 138pp; English.

XX The present invention describes (A) an isolated HIV-1 Group O env
 CC polypeptide. Also described are: (1) an isolated HIV-1 group O env
 CC polypeptide comprising an immunorecognition epitope as in
 CC (A); (2) a polypeptide comprising a first HIV-1 Group O env polypeptide
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct
 CC comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env
 CC polypeptide, and at least one additional HIV-1 polypeptide; (6) a
 CC antigen construct comprising a first HIV-2 env polypeptide fused to a
 CC second HIV-2 env polypeptide comprising an expression vector as in (8); (9) a
 CC host cell transformed by an expression vector comprising a PN as in (7); (9) a
 CC immunosay kit for the detection of antibodies to HIV-1 comprising an
 CC antigen construct as in (3)-(6). The antigen constructs can be used for
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be
 CC used as immunogens to produce antibodies. The antibodies can be used to
 CC purify HIV polypeptides, for therapy and for detection of HIV
 CC polypeptides.

XX Sequence 215 AA:

Query Match .91.5%; Score 161; DB 20; Length 215;
 Best Local Similarity 84.4%; Pred. No. 6, 5e-14;
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

XX 1 ALETTLNOQLNSMGCRGLVCTYSVRFNET 32
 117 aletllngqlnlhwgcgrllcytstvkwmet 148

RESULT 7
 Y06983 106983 standard: Protein: 215 AA.
 AC Y06983:
 DT 06-JUL-1999 (first entry)
 XX Recombinant pCO-8pL protein.
 DE HIV-1: HIV-2: Immobilised capture reagent; capillary action; screening;
 XX antibody; assay.
 KM HIV-1: HIV-2: Immobilised capture reagent; capillary action; screening;
 KM antibody; assay.
 OS Human immunodeficiency virus type 1.
 XX Key Location/Qualifiers
 FH Protein 2..46 "gp120 sequence"
 FT /note= "47..245"
 FT Peptide /note= "gp41 sequence"
 XX

PN W09090410-A2.
 XX 25-FEB-1999.
 PD 07-AUG-1998; 98MO-US16506.
 PF 15-AUG-1997; 97US-0912129.
 PR (ABBO) ABBOTT LAB.
 XX Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;
 PI Necklows EC, Vallari AS, Varilek V;
 DR WPI: 1999-190224/16.
 DR N-PSDB: X37193.
 XX New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -
 PT can be used in field assay, requiring no electricity and less
 PT specialised equipment
 PS Claim 1; Fig 5; 104pp; English.

XX The invention relates to a rapid assay for simultaneous detection and
 CC differentiation of antibodies to HIV-1 groups O and M, and identifying at
 CC method comprises (a) contacting the sample analyte and on which the sample
 CC least one immobilised capture reagent to the distal end by capillary action, under
 CC conditions sufficient to form capture reagent/analyte complexes, and
 CC (b) determining the presence of analyte(s) by detecting a visible colour
 CC change at the capture reagent site on the strip wherein the capture
 CC reagent for HIV-1 group O comprises a polypeptide shown in Y06977-80 and
 CC Y06983-84; and that for HIV-2 comprises a polypeptide Y06981. The
 CC invention is used to detect antibodies to HIV-1 groups O and
 CC HIV-2. The invention will be particularly useful in places and
 CC situation where equipment and/or electricity is not available. The
 CC equipment provides a screening method which is faster and requires less
 CC capture reagent than prior art methods. The present sequence represents a
 CC amino acid sequence of the recombinant pCO-8pL protein which acts as a
 CC capture reagent for HIV-1 group O.
 XX Sequence 215 AA:

Query Match .91.5%; Score 161; DB 20; Length 215;
 Best Local Similarity 84.4%; Pred. No. 6, 5e-14;
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

XX 1 ALETTLNOQLNSMGCRGLVCTYSVRFNET 32
 117 aletllngqlnlhwgcgrllcytstvkwmet 148

RESULT 8
 Y77374 Y77374 standard: Protein: 215 AA.
 AC Y77374:
 DT 22-MAY-2000 (first entry)
 XX HIV-1 group O env gp120/gp41 pCO-8pL recombinant protein, SEQ ID NO:58.
 DE HIV-1 group O: env; gp120; gp41; glycoprotein; monoclonal antibody;
 XX immunosay; positive control; affinity purification; therapeutic;
 KM Escherichia coli; antigen; synthetic gene construction; mutagen;
 KM deletion mutation.
 OS Human immunodeficiency virus type 1 group O isolate HAM112.
 XX Synthetic.
 PN W0200004383-A2.

FT Protein 2..46
 FT /note= "gp120 sequence"
 FT 47..245
 FT Peptide /note= "gp41 sequence"
 XX
 XX W09909410-42.
 XX
 XX 25-FEB-1999.
 XX
 XX 07-AUG-1998: 98WO-US156506.
 XX
 XX 15-AUG-1997: 97US-0912129.
 XX
 XX (ABRO) ABBOTT LAB.
 XX Brennan CA, Devare SG, Golden AM, Hackett JF, Hickman RK;
 XX Necklaws EC, Vallari AS, Varlick V;
 XX WPI: 1999-190224/16.
 XX N-PSDB: X37189.
 DR
 PT New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -
 PT can be used for a rapid assay, requiring no electrophoresis and less
 PT specialized equipment
 PS
 PS Claim 1: Fig 7: 104pp: English.
 XX
 XX The invention relates to a rapid assay for simultaneous detection and
 XX differentiation of antibodies to HIV-1 groups O and M, and containing at
 XX least one antibody to HIV-1 group O antigen and one antibody to HIV-1
 XX group M antigen, the assay being performed by a method in which the sample
 XX moves from the proximal to the distal end by capillary action, under
 XX conditions sufficient to form capture reagent/antigen complexes, and
 XX (b) determining the presence of analyte(s) by detecting a visible colour
 XX change at the capture reagent site on the strip wherein the capture
 XX reagent for HIV-1 group O comprises a polypeptide shown in FIGS 60 and
 XX 105983-84; and that for HIV-1 group M the polypeptide shown in FIGS 60 and
 XX 105982-83, and that for HIV-1 group M the polypeptide shown in FIGS 60 and
 XX 105982-83, and that for HIV-1 group M the polypeptide shown in FIGS 60 and
 XX M, and HIV-2. The invention will be particularly useful in places and
 XX CC situation where equipment and/or electricity is not available. The
 XX CC invention provides a screening method which is faster and requires less
 XX CC equipment than prior art methods. The present sequence represents a
 XX CC amino acid sequence of the recombinant pG0-9PL recombinant protein which
 XX CC acts as a capture reagent for HIV-1 group O.
 XX
 XX Sequence 245 AA:
 SO
 Query Match 91.5%: Score 161; DB 20; Length 245;
 Best Local Similarity 84.4%: Pred. No. 7, 5e-14;
 Matches 27: Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 OY 1 ALETLIDNOOLLNSGRCGRGLCTYSWRNRET 32
 DB 117 aletlignqllhwgckgrlcytsvknwt 148
 RESULT 11
 Y77369 77369 standard; Protein: 245 AA.
 XX Y77369:
 XX 22-MAY-2000 (first entry)
 XX
 XX HIV-1 group O pG0-9PL-encoded truncated env gp41 protein. SEQ ID NO:48.
 XX
 XX HIV-1 group O; env: gp120; gp41: glycoprotein; monoclonal antibody;
 XX immunosay: positive control; affinity purification; therapeutic;
 XX Bacetricha coli; antigen; synthetic gene construction; mutagen;
 XX deletion mutation.
 XX

OS Human immunodeficiency virus type 1 group O isolate HAN112.
 XX Synthetic.
 XX W0200004383-42.
 XX
 XX 27-JAN-2000.
 XX
 XX 09-JUL-1999: 99WO-US15469.
 XX
 XX 14-JUL-1998: 98US-0115171.
 XX
 XX (ABRO) ABBOTT LAB.
 XX
 XX Scheffell JW, Hackett JF, Tyner JD, Hickman RK;
 XX WPI: 2000-171290/15.
 XX N-PSDB: Z90280.
 DR
 PT Novel monoclonal antibodies useful as positive control reagent for
 PT detecting human immunodeficiency virus infections and diagnosing,
 PT evaluating or prognosing viral disease -
 PS
 PS Example 3: Page 120-121; 148pp: English.
 XX
 XX The invention relates to anti-HIV-1 group O monoclonal antibodies, which
 XX may be used as positive control reagents in immunoassays to detect and
 XX differentiate HIV-1 group O infections. The invention also encompasses a
 XX differential antibody which binds specifically to an HIV-1 group O antigen,
 XX which has no more than 15% cross reactivity to a corresponding antigen
 XX selected from HIV-1 group M antigens and HIV-2 antigens; and a method of
 XX using a monoclonal antibody as a positive control reagent in an
 XX immunoassay for the detection of anti-HIV-1 group O antibodies. The
 XX monoclonal antibodies are useful as positive control reagents in such
 XX immunoassays capable of coupling a monoclonal antibody with HIV group-1
 XX antigen and detecting the antigen-antibody complex. The monoclonal
 XX antibodies of the invention would be used to ensure that the reagents
 XX provided to detect HIV-1 group O antibody were performing properly. The
 XX monoclonal antibodies may also can be immobilised on a matrix and used
 XX for affinity purification of specific HIV-1 group O antibodies. The
 XX cell cultures or biological tissues and fluids for therapeutic use. Different
 XX CC epitopes of HIV antigens can be used in combination to identify different
 XX CC epitopes, or prognosticate HIV disease condition. The monoclonal
 XX CC antibodies are also useful for differentiating HIV-1 Group O antigens
 XX CC from HIV-group M and HIV-2 antigens. Sequences Y77369-Y77375 represent
 XX CC recombinant HIV-1 group O env antigens encoded by the synthetic genes
 XX CC Z90280-Z90286. The recombinant HIV-1 group O proteins (Y77376). The
 XX CC deletions relative to the HIV-1 group O antigens were purified and used to screen
 XX CC recombinant HIV-1 group O antigens were purified and used to screen
 XX CC hybridoma cultures.
 XX
 XX Sequence 245 AA:
 SO
 Query Match 91.5%: Score 161; DB 21; Length 245;
 Best Local Similarity 84.4%: Pred. No. 7, 5e-14;
 Matches 27: Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 OY 1 ALETLIDNOOLLNSGRCGRGLCTYSWRNRET 32
 DB 117 aletlignqllhwgckgrlcytsvknwt 148
 RESULT 12
 Y09507 109507 standard; Protein: 281 AA.
 XX Y09507:
 XX 15-JUL-1999 (first entry)
 XX

[illegible]

XX	
OS	Human immunodeficiency virus type 1.
XX	
XX	W09090179-A2.
XX	
PD	25-FEB-1999.
XX	
XX	
PE	17-AUG-1998; 98MO-USI7014.
XX	
XX	15-AUG-1997; 97US-0911824.
XX	
PA	(ABBO) ABBOT LAB.
P1	
X1	Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J,
DR	WPJ. 1999-180167/16.
XX	
DR	N-FSDB; X56076.
XX	
XX	
PT	New Isolated HIV-1 Group Q env polypeptides - used for the
PT	detection of anti-HIV antibodies and for the production of
PT	antibodies for use in detection, purification and therapy
XX	
XX	Claim 15; Fig 9; 138pp; English.

[illegible]

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FH Key Location/Qualifiers
FT Protein 2..46
FT /note="gp120 sequence"
FT Peptide 47..245 "gp41 sequence"
FT /note="gp41 sequence"
PN MO9909410-A2.
PD 25-FEB-1999.
PF 07-AUG-1998: 98MO-US16506.
PR 15-AUG-1997: 97US-0912129.
PX (ABRO) ABBOTT LAB.
PY Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK,
PI Necklans EC, Vallier AS, Varilek V.
PI
XX WPI: 1999-190234/16.
XX N-PSDB: X37191.

PT New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -
PT can be used in field assay, requiring no electricity and less
PT specialised equipment
PT
XX Claim 1: Fig 9: 104pp: English.
XX
XX The invention relates to a rapid assay for simultaneous detection and
XX differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The
XX differentiation is achieved by contacting the sample with a strip containing at
XX least one immobilised capture reagent per analyte and on which the sample
XX moves from the proximal to the distal end by capillary action, under
XX conditions sufficient to form capture reagent/analyte complexes, and
XX (b) determining the presence of analyte(s) by detecting a visible colour
XX change at the capture reagent site on the strip wherein the capture
XX reagent for HIV-1 group O comprises a polypeptide of amino acid sequence
XX Y06982, 84, 4 that for HIV-2 comprises the polypeptide shown in Y06981. The
XX invention is used to screen patients for antibodies to HIV-1 types O and
XX M, and HIV-2. The invention will be particularly useful in places and
XX situation where equipment and/or electricity is not available. The
XX invention provides a screening method which is faster and requires less
XX equipment than prior art methods. The present sequence represents a
XX amino acid sequence of the recombinant pCO-11pV recombinant protein which
XX acts as a capture reagent for HIV-1 group O.
XX
XX Sequence 373 AA:
XX
XX Query Match 91.5%; Score 161; DB 20; Length 373;
XX Best Local Similarity 84.4%; Pred. NO. 1.2e-13;
XX Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 ALETLQNDQLNSGCRGRVCTTSYRNFT 32
XX |||||.....|.....|.....|.....|
XX DB 117 aletlqngllhgwckgrtllcysskxmet 148

RESULT 15
Y09500 ID Y09500 standard; Protein: 460 AA.
XX
XX Y09500:
XX
XX 15-JUL-1999 (first entry)
XX
XX HIV-1 Group O env polypeptide pCO-8CKS.
XX
XX HIV; human Immunodeficiency virus; antigen; detection; antibody;
XX differentiation; Group O; env; Immunogen; Immunassay.
XX
XX Human Immunodeficiency virus type 1.
XX

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XX MO9909179-A2.
XX 25-FEB-1999.
XX
XX 17-AUG-1998: 98MO-US17014.
XX
XX 15-AUG-1997: 97US-0911824.
XX
XX (ABRO) ABBOTT LAB.
XX
XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J.
XX WPI: 1999-190167/16.
XX N-PSDB: X56079.

PT New isolated HIV-1 Group O env polypeptides - used for the
PT detection of anti-HIV antibodies and for the production of
PT antibodies for use in detection, purification and therapy
PT
XX Example 3: Fig 6: 138pp: English.
XX
XX The present invention describes (A) an isolated HIV-1 Group O env
XX polypeptide. Also described are: (1) an isolated HIV-1 Group O env
XX polypeptide comprising an immunoreactive portion of a polypeptide as in
XX (A); (2) a polynucleotide (PN) encoding a HIV-1 Group O env polypeptide
XX (A); an antigen construct (AC) comprising a HIV-1 Group O env polypeptide
XX comprising a fusion of at least one HIV-1 Group O env polypeptide with at
XX least one HIV-1 Group M env polypeptide; (5) an antigen construct
XX comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env
XX polypeptide, and at least one additional HIV-1 polypeptide; (6) an
XX antigen construct comprising a first HIV-2 env polypeptide; (8) an
XX second HIV-2 env polypeptide; (9) an antigen construct comprising a
XX first HIV-2 env polypeptide and a second HIV-2 env polypeptide as
XX in (9); (10) a fusion protein formed by an expression vector as in (8); and (10) an
XX immunosay kit for the detection of antibodies to HIV-1 comprising an
XX antigen construct as in (3)-(6). The antigen constructs can be used for
XX the detection of anti-HIV-1 antibodies in test samples. They can also be
XX used as immunogens to produce antibodies. The antibodies can be used to
XX purify HIV polypeptides, for therapy and for detection of HIV
XX polypeptides.
XX
XX Sequence 460 AA:
XX
XX Query Match 91.5%; Score 161; DB 20; Length 460;
XX Best Local Similarity 84.4%; Pred. NO. 1.5e-13;
XX Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 ALETLQNDQLNSGCRGRVCTTSYRNFT 32
XX |||||.....|.....|.....|.....|
XX DB 362 aletlqngllhgwckgrtllcysskxmet 393

Search completed: March 22, 2001, 09:51:53
Job time: 71 sec

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Fri Mar 23 07:47:24 2001

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Page 9

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GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OK NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BCF1;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RL type 1 group O.*";
RM Philippe M., Robertson D., Sandline S., Christel D., Francois S.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.*";
DR submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
FT ENBL_AJ236404; CAB96252.1;
FT NON_TER 1 1
FT SEQUENCE 219 AA: 25353 MW; F65829EB01520D91 CRC64;
SQ
Query Match 92.6%; Score 163; DB 12; Length 219;
Best Local Similarity 87.5%; Pred. No. 9e-17;
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 1 ALETLQNDOLNLSMCKGRGLVCTSVKNNET 32
1 ALETLQNDOLNLSMCKGRGLVCTSVKNNET 78
|||||:|||||:|||||:|||||:|||||:
RESULT 3
ID 09IHU7 PRELIMINARY; PRT; 124 AA.
AC 09IHU7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OK NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=97MH06;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RL type 1 group O.*";
RM AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR ENBL_AJ229237; AAF71914.1;
FT NON_TER 1 1
FT SEQUENCE 124 AA: 15187 MW; 105D515F114450F8 CRC64;
SQ
Query Match 91.5%; Score 161; DB 12; Length 124;
Best Local Similarity 84.4%; Pred. No. 9.1e-17;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Db 1 ALETLQNDOLNLSMCKGRGLVCTSVKNNET 32
1 ALETLQNDOLNLSMCKGRGLVCTSVKNNET 54
|||||:|||||:|||||:|||||:|||||:
RESULT 4
ID 09IHV1 PRELIMINARY; PRT; 126 AA.
AC 09IHV1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OK NCBI_TaxID=11676;

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RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=97J5203;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RL type 1 group O.*";
RM AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR ENBL_AJ229233; AAF71910.1;
FT NON_TER 1 1
FT SEQUENCE 126 AA: 15169 MW; 13B101EDCCF0DD0 CRC64;
SQ
Query Match 91.5%; Score 161; DB 12; Length 126;
Best Local Similarity 87.5%; Pred. No. 9.3e-17;
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 1 ALETLQNDOLNLSMCKGRGLVCTSVKNNET 32
1 ALETLQNDOLNLSMCKGRGLVCTSVKNNET 61
|||||:|||||:|||||:|||||:|||||:
RESULT 5
ID 09IHU9 PRELIMINARY; PRT; 130 AA.
AC 09IHU9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OK NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=97CM798;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RL type 1 group O.*";
RM AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR ENBL_AJ229233; AAF71912.1;
FT NON_TER 1 1
FT SEQUENCE 130 AA: 15593 MW; 5B85789A36344EA CRC64;
SQ
Query Match 91.5%; Score 161; DB 12; Length 130;
Best Local Similarity 84.4%; Pred. No. 9.6e-17;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Db 1 ALETLQNDOLNLSMCKGRGLVCTSVKNNET 32
1 ALETLQNDOLNLSMCKGRGLVCTSVKNNET 61
|||||:|||||:|||||:|||||:|||||:
RESULT 6
ID 09IHR3 PRELIMINARY; PRT; 172 AA.
AC 09IHR3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OK NCBI_TaxID=11676;
RP SEQUENCE FROM N.A.
RA STRAIN=BCF99;

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RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 RA Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.*;
 RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL:AF236407; CAB96255.1;
 FT NON_TER
 FT NON_TER 172 172
 SO SEQUENCE 172 AA; 20388 MW; 972CAFA2A7546B13 CRC64;

Query Match 91.5%; Score 161; DB 12; Length 172;
 Best Local Similarity 84.4%; Pred. No. 1,3e-16;
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQQOOLLNSMCGRGRLCYTSVNMNF 32
 DB 26 ALETLIQQOOLLNSMCGRGRLCYTSVNMNF 57

RESULT 7
 AC 09IEB2 PRELIMINARY; PRT; 234 AA.
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE GP41 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=BCP100;
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 RA Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.*;
 RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL:AF236357; CAB96146.1;
 FT NON_TER
 FT NON_TER 234 234
 SO SEQUENCE 234 AA; 27036 MW; 39B050B3F855A8C CRC64;

Query Match 91.5%; Score 161; DB 12; Length 234;
 Best Local Similarity 84.4%; Pred. No. 1,7e-16;
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQQOOLLNSMCGRGRLCYTSVNMNF 32
 DB 48 ALETLIQQOOLLNSMCGRGRLCYTSVNMNF 79

RESULT 8
 AC 09IEB2 PRELIMINARY; PRT; 240 AA.
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE TM, GP41 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=BCP111;
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 RA Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.*;
 RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL:AF243365; CAB96335.1;

FT NON_TER 1 1
 FT NON_TER 240 240
 SO SEQUENCE 240 AA; 27723 MW; 1E2065B0491A197 CRC64;

Query Match 90.9%; Score 160; DB 12; Length 240;
 Best Local Similarity 84.4%; Pred. No. 2,5e-16;
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQQOOLLNSMCGRGRLCYTSVNMNF 32
 DB 50 ALETLIQQOOLLNSMCGRGRLCYTSVNMNF 81

RESULT 9
 ID 09IH08 PRELIMINARY; PRT; 125 AA.
 AC 09IH08;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN GP41.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=57CM766;
 RA Vain C, Oso F., Rodriguez P.N., Zekeng L., van der Groen G.,
 RA Plataszek D., Scheldt C.;
 RA *Phylogenetic analysis of protease and transmembrane regions of HIV
 RT type 1 group O.*;
 DR AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
 RL EMBL:AF229236; AF271913.1;
 FT NON_TER
 FT NON_TER 125 125
 SO SEQUENCE 125 AA; 15108 MW; EA2896C4B25F342 CRC64;

Query Match 90.3%; Score 159; DB 12; Length 125;
 Best Local Similarity 81.2%; Pred. No. 1,8e-16;
 Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQQOOLLNSMCGRGRLCYTSVNMNF 32
 DB 27 ALETLIQQOOLLNSMCGRGRLCYTSVNMNF 58

RESULT 10
 ID 09IEA5 PRELIMINARY; PRT; 216 AA.
 AC 09IEA5;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE GP41 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=IEF26;
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 RA Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.*;
 RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL:AF236445; CAB96263.1;
 FT NON_TER
 FT NON_TER 216 216
 SO SEQUENCE 216 AA; 25003 MW; 0A5AC21BBFA88932 CRC64;

Query Match 90.38; Score 159; DB 12; Length 216;

Best Local Similarity 87.58; Pred. No. 3,1e-16; Matches 28; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLNSMCKGRGLVCTSVKNNKT 32
DB 32 ALETLIONOOLLNSMCKGRGLVCTSVKNNKT 63

RESULT 11

OY01E31 PRELIMINARY; PRT; 242 AA.

AC G01E31-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
EN TM, GP41 (FRAGMENT).

GN ENV.

Human Immunodeficiency virus type 1.

Viruses; Retroviral viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

RA Deplenne C., Brun-Vezinet F., Dormont D., Simon F.O.;
RT "Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ243366; CAB96366.1;

FT NON-TER 242

SEQUENCE 242 AA: DEBA73DF0E8A6ED7 CRC64;

Query Match 90.38; Score 159; DB 12; Length 242;

Best Local Similarity 81.28; Pred. No. 3.5e-16; Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLNSMCKGRGLVCTSVKNNKT 32
DB 54 ALETLIONOOLLNSMCKGRGLVCTSVKNNKT 85

RESULT 12

OY01E09 PRELIMINARY; PRT; 544 AA.

AC G01E09-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
EN ENV.

Human Immunodeficiency virus type 1.

Viruses; Retroviral viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

RA Deplenne C., Brun-Vezinet F., Dormont D., Simon F.O.;
RT "Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates";
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF229229; CAB96229.1;

FT NON-TER 544

SEQUENCE 544 AA: FC3CF4E31D86D50 CRC64;

Query Match 90.38; Score 159; DB 12; Length 544;

Best Local Similarity 87.58; Pred. No. 7.7e-16; Matches 28; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLNSMCKGRGLVCTSVKNNKT 32
DB 360 ALETLIONOOLLNSMCKGRGLVCTSVKNNKT 391

RESULT 13

OY04059 PRELIMINARY; PRT; 116 AA.

AC G04059-1998 (TREMBLrel. 05, Created)
DT 01-MAY-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
EN ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).

OS Human Immunodeficiency virus type 1.

Viruses; Retroviral viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

RA Billetier-Bache F., Ekas E., Peeters M., Delaporte E.;
RT Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.

DR EMBL: Y09775; CAAT0914.1;

DR INTERPRO: IPR000328;

DR PFAM: PF00517; GP41.1;

FT NON-TER 116

SEQUENCE 116 AA: 13975 MW: 12B3D0DD02A1D32 CRC64;

Query Match 89.88; Score 138; DB 12; Length 116;

Best Local Similarity 84.48; Pred. No. 2.4e-16; Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLNSMCKGRGLVCTSVKNNKT 32
DB 29 ALETLIONOOLLNSMCKGRGLVCTSVKNNKT 60

RESULT 14

OY01HV5 PRELIMINARY; PRT; 137 AA.

AC G01HV5-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
EN ENVELOPE GLYCOPROTEIN (FRAGMENT).

OS Human Immunodeficiency virus type 1.

Viruses; Retroviral viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

RA Yang C., Gao F., Fongjunga P.N., Zekeng L., van der Groen G.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV type 1 group O retroviruses 16.1075-1081 (2000).";
RL EMBL: AF229229; AAF71906.1;

FT NON-TER 137

SEQUENCE 137 AA: 16494 MW: 55C4709608168493 CRC64;

Query Match 89.88; Score 158; DB 12; Length 137;

Best Local Similarity 84.48; Pred. No. 2.9e-16; Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLNSMCKGRGLVCTSVKNNKT 32
DB 30 ALETLIONOOLLNSMCKGRGLVCTSVKNNKT 61


```

RESULT 15
Q9TEA3
ID Q9TEA3 PRELIMINARY; PT: 208 AA.
NC Q9TEA3:2000 (FEBMRL1.15, Created)
DT 01-OCT-2000 (FEBMRL1.15, Last sequence update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid:11676;
RN 11
RC SOURCE FROM N.A.
RC STOUV:1999
RA Philippe M.;
RA Roberton D., Sandrine S., Christel D., Francois S.,
RA "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AJ236417; CAB6265.1;
NON_TER 1
FT 208 1
SQ SEQUENCE 208 AA: 24286 MW: 102961C1935A07A1 CRC64;

```

```

Query Match 89.88; Score 158; DP 12; Length 208;
Best Local Similarity 81.28; Pred. No. 4,3e-16;
Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
OY 1 ALETLNQNQGLNSWCGRCGRGLVCTSVANMET 32
DB 24 ALETLNQNQGLNSWCGRCGRGLVCTSVANMET 55

```

Search completed: March 22, 2001, 10:00:46
Job time: 525 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:57:49 ; Search time 29.4 seconds

(without alignments)

Title: US-09-147-362-11

```

perfect score: 1/0
Sequence:      1 ALETLNOLLNSWGCGRGLVCTSVRWNET 32

```

Scoring table: BLOSUM62

Searched: 88757 seqs, 32294092 residues

total number of hits satisfying chosen parameters:

```

Minimum DB seq length: 0
Maximum DB seq length: 3000000000

```

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:★

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	110	62.5	854	1	ENV_STV2C	P1721 chimpanzee
2	103	58.5	853	1	ENV_HV12Z	P12487 human
3	103	58.5	855	1	ENV_HV12G	P14580 human
4	102	58.0	843	1	ENV_HV12I	P35961 human
5	102	58.0	847	1	ENV_HV1S1	P19550 human
6	102	58.0	847	1	ENV_HV12W	P05880 human
7	102	58.0	851	1	ENV_HV12B	P04582 human
8	102	58.0	851	1	ENV_HV1S3	P12448 human
9	102	58.0	852	1	ENV_HV1S5	P19549 human
10	102	58.0	852	1	ENV_HV1M6	P19551 human
11	102	58.0	852	1	ENV_HV1G2	P03378 human
12	102	58.0	855	1	ENV_HV1B1	P20888 human
13	102	58.0	856	1	ENV_HV1B2	P04575 human
14	102	58.0	856	1	ENV_HV1L4	P04576 human
15	102	58.0	856	1	ENV_HV1L5	Q70656 human
16	102	58.0	856	1	ENV_HV1M4	P05877 human
17	102	58.0	856	1	ENV_HV1P4	P03376 human
18	102	58.0	856	1	ENV_HV1P5C	P05878 human
19	102	58.0	861	1	ENV_HV1M1	P131872 human
20	102	58.0	861	1	ENV_HV1B1	P03377 human
21	102	58.0	867	1	ENV_HV1B3	P04579 human
22	102	58.0	867	1	ENV_HV1J3	P12489 human
23	102	58.0	868	1	ENV_HV1C4	P05879 human
24	100	56.8	858	1	ENV_HV1J4	P20871 human
25	100	56.8	858	1	ENV_HV1J5	P04654 human
26	100	56.8	856	1	ENV_HV1J6	P05881 human
27	100	56.2	846	1	ENV_HV1Z8	P05882 human
28	98	55.7	863	1	ENV_HV1Z8	P04581 human
29	98	54.5	853	1	ENV_HV1ZL	P05883 human
30	96	54.5	856	1	ENV_HV1ZB	P13181 human
31	95.5	54.3	856	1	ENV_HV1ZB	P05883 human
32	95.5	54.3	859	1	ENV_HV1ZD	P15831 human
33	95.5	54.3	885	1	ENV_STV54	P12492 simian

34	95	54.0	857	1	ENV_HVZKR	074126	human	Immature
35	94	53.4	858	1	ENV_HVZGL	P04377	human	Immature
36	94	53.4	859	1	ENV_HVYAM	P05883	human	Immature
37	93	52.8	865	1	ENV_HVYAT	slr1448	human	Immature
38	92.5	52.6	712	1	ENV_HVZS2	P23536	human	Immature
39	92.5	52.6	859	1	ENV_HVZS2	P20872	human	Immature
40	91.5	52.0	859	1	ENV_HVZCA	P24105	human	Immature
41	91	51.7	854	1	ENV_HVYAT	O02837	human	Immature
42	90.5	51.4	846	1	ENV_HVZGB	P12449	human	Immature
43	90	51.4	821	1	ENV_HVZS8	P22380	human	Immature
44	90	51.1	851	1	ENV_HVZD1	P17755	human	Immature
45	90	51.1	851	1	ENV_HVZG1	P18040	human	Immature

ALIGNMENTS

[illegible]

Query Match	Similarity	Score	DB 1:	Length
Best Local	53.1%	58.5%	Score 103:	DB 1: 853:
Matches 1/:	Conservative	7:	Mis-Matches 8:	Indels 0:
Db	579	AVERYLKDQQLLGLMGCSGKLCITTVTPWSS	610	0:
Oy	1	ALETLLDNOLNLSMCSNRCVCTSYRHNPT	32	0:
Id	1	ENY_HV126	STANDARD:	855 AA.
RN	1	ENY_HV126	STANDARD:	855 AA.
NC	1	P03450	1987 (rel. 05. Created)	
DT	13-AUG-1987 (rel. 05. Last annotation update)			
DE	15-JUL-1999 (rel. 38. Last annotation update)			
ENVELOPE POLYPEPTIDE GL10 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).				
GN	ENV.			
DE	Human Immunodeficiency virus type 1 (zai1e 6 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
RN	1	SEQUENCE FROM N.A.		
DT	13-AUG-1987 (rel. 05. Created)			
DE	15-JUL-1999 (rel. 38. Last annotation update)			
ENVELOPE POLYPEPTIDE GL10 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).				
GN	ENV.			
DE	Human Immunodeficiency virus type 1 (zai1e 6 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
RN	1	SEQUENCE FROM N.A.		
DT	13-AUG-1987 (rel. 05. Created)			
DE	15-JUL-1999 (rel. 38. Last annotation update)			
ENVELOPE POLYPEPTIDE GL10 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).				
GN	ENV.			
DE	Human Immunodeficiency virus type 1 (zai1e 6 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
RN	1	SEQUENCE FROM N.A.		
DT	13-AUG-1987 (rel. 05. Created)			
DE	15-JUL-1999 (rel. 38. Last annotation update)			
ENVELOPE POLYPEPTIDE GL10 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).				
GN	ENV.			
DE	Human Immunodeficiency virus type 1 (zai1e 6 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
RN	1	SEQUENCE FROM N.A.		
DT	13-AUG-1987 (rel. 05. Created)			
DE	15-JUL-1999 (rel. 38. Last annotation update)			
ENVELOPE POLYPEPTIDE GL10 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).				
GN	ENV.			
DE	Human Immunodeficiency virus type 1 (zai1e 6 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
RN	1	SEQUENCE FROM N.A.		
DT	13-AUG-1987 (rel. 05. Created)			
DE	15-JUL-1999 (rel. 38. Last annotation update)			
ENVELOPE POLYPEPTIDE GL10 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).				
GN	ENV.			
DE	Human Immunodeficiency virus type 1 (zai1e 6 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
RN	1	SEQUENCE FROM N.A.		
DT	13-AUG-1987 (rel. 05. Created)			
DE	15-JUL-1999 (rel. 38. Last annotation update)			
ENVELOPE POLYPEPTIDE GL10 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).				
GN	ENV.			
DE	Human Immunodeficiency virus type 1 (zai1e 6 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
RN	1	SEQUENCE FROM N.A.		
DT	13-AUG-1987 (rel. 05. Created)			
DE	15-JUL-1999 (rel. 38. Last annotation update)			
ENVELOPE POLYPEPTIDE GL10 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).				
GN	ENV.			
DE	Human Immunodeficiency virus type 1 (zai1e 6 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
RN	1	SEQUENCE FROM N.A.		
DT	13-AUG-1987 (rel. 05. Created)			
DE	15-JUL-1999 (rel. 38. Last annotation update)			
ENVELOPE POLYPEPTIDE GL10 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).				
GN	ENV.			
DE	Human Immunodeficiency virus type 1 (zai1e 6 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
RN	1	SEQUENCE FROM N.A.		
DT	13-AUG-1987 (rel. 05. Created)			
DE	15-JUL-1999 (rel. 38. Last annotation update)			
ENVELOPE POLYPEPTIDE GL10 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).				
GN	ENV.			
DE	Human Immunodeficiency virus type 1 (zai1e 6 isolate) (HIV-1).			
OC				

DR INTERPRO: IPR000328; -
 DR INTERPRO: IPR000777; -
 DR PFM: PF00516; GP41; 1.
 DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KM SIGNAL
 FT CHAIN 1 30
 FT CHAIN 31 510
 FT CHAIN 511 855
 FT DISULFID 53 73
 FT DISULFID 118 207
 FT DISULFID 125 198
 FT DISULFID 130 155
 FT DISULFID 132 249
 FT DISULFID 220 332
 FT DISULFID 298 444
 FT DISULFID 378 417
 FT DISULFID 385 417
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 140 140
 FT CARBOHYD 145 145
 FT CARBOHYD 154 154
 FT CARBOHYD 186 186
 FT CARBOHYD 189 189
 FT CARBOHYD 199 199
 FT CARBOHYD 236 236
 FT CARBOHYD 243 243
 FT CARBOHYD 264 264
 FT CARBOHYD 278 278
 FT CARBOHYD 297 297
 FT CARBOHYD 333 333
 FT CARBOHYD 340 340
 FT CARBOHYD 355 355
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 FT CARBOHYD 461 461
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 FT CARBOHYD 610 610
 FT CARBOHYD 615 615
 FT CARBOHYD 636 636
 FT CARBOHYD 673 673
 SO SEQUENCE 855 AA; 96971 MW; 384036239C457 CR64;
 Query Match 58.5%; Score 103; DB 1; Length 855;
 Best Local Similarity 53.1%; Pred. No. 2, 6e-07;
 Matches 17; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
 OY 1 ALSTLIQDQILNSMCGRCGRINCYTSYNNH 32
 DB 581 AVERYLKQDQLGIMSGSKLCTTPVNNSS 612
 RESULT 4
 ID ENV HY12 STANDARD: PFM: 843 AA.
 AC P35961;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
 DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
 ENV.
 OS Human immunodeficiency virus type 1 (Yu-2 isolate) (HIV-1).

CC VIRUSES; Retroviral viruses; Retroviridae; Lentivirus.
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9302387; PubMed-1404605;
 RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
 Shaw G.M.;
 RT *Complete nucleotide sequence, genome organization, and biological
 RT properties of human immunodeficiency virus type 1 in vivo: evidence
 RT for limited defectiveness and complementation.*;
 RL J. Virol. 66:6587-6600(1992).
 CC The SWISS-PROT entry is a protein of 160 amino acids. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no known mutations on this
 CC use by non-profit institutions as long as its content is not used for
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 CC entities requires a license agreement (See <http://www.slb.ch/announce/>
 CC or send an email to license@slb.ch).
 DR PFM: M0358; NOT_ANNOTATED_CDS.
 DR PFM: H4400; H4400;
 DR INTERPRO: IPR000328; -
 DR INTERPRO: IPR000777; -
 DR PFM: PF00516; GP120; 1.
 DR PFM: PF00517; GP41; 1.
 KM AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KM SIGNAL
 FT CHAIN 1 30
 FT CHAIN 31 429
 FT CHAIN 430 843
 FT CHAIN 490 843
 FT CHAIN 738 755
 FT TRANSMEM 738 755
 FT DISULFID 53 73
 FT DISULFID 118 201
 FT DISULFID 125 192
 FT DISULFID 130 155
 FT DISULFID 132 245
 FT DISULFID 214 325
 FT DISULFID 292 325
 FT DISULFID 373 432
 FT DISULFID 380 405
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 135 135
 FT CARBOHYD 138 138
 FT CARBOHYD 158 158
 FT CARBOHYD 184 184
 FT CARBOHYD 193 193
 FT CARBOHYD 230 230
 FT CARBOHYD 237 237
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 FT CARBOHYD 598 598
 FT CARBOHYD 603 603
 FT CARBOHYD 612 612
 FT CARBOHYD 624 624
 FT CARBOHYD 803 803
 FT CARBOHYD 803 803
 SO SEQUENCE 843 AA; 95648 MW; C69DBD971DC918B71 CR64;
 Query Match 58.0%; Score 102; DB 1; Length 843;
 Best Local Similarity 56.7%; Pred. No. 3, 6e-07;

FT	CARDOND	140	140	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	151	151	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	155	155	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	183	183	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	184	184	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	194	194	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	211	211	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	239	239	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	259	259	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	273	273	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	286	286	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	292	292	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	317	317	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	327	327	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	350	350	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	356	356	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	380	380	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	386	386	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	390	390	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	400	400	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	438	438	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	458	458	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	602	602	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	607	607	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	616	616	N-LINKED	(GLNAC	-)	(POTENTIAL)
FT	CARDOND	628	628	N-LINKED	(GLNAC	-)	(POTENTIAL)
Q2	SEQUENCE	847 AA:	94666 MW:	C1E0377A45BCDA	CRC64:		

Qy 1 ALETTLLNOQLINSWCGRRLWCYTSVRRN 30
 |:| :::||| | | :|:| :| |
Db 573 AVERYLRIQQDLGIMGSGKILCTTTPPNN 602

PP SEQUENCE FROM N. A. Pubmed-2578615.
RX MEDLINE-05111123.
RA Ratner L, Haseltine W, Patarca R, Livak K.J., Starich B.R.,
RA Josephs S.F., Doran E.R., Raskaski J.A., Whitehead
RA Baumeister K., Yanoof I.L., Peltway S.R., Johnson
RA Lautenberger J.A., Papas T.S., Chiryaev J., Chang N.T., Gallo R.C.
RA Wong-Staal F.
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III".

RL Nature 313:277-284(1985).
 CC
 CC This Swiss-patented copyright. It is produced through a collaboration
 CC between the Swiss Patent Office, Bioinformatics and the EMBL outstation
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 CC or send an email to license@slb.stb.ch).
 DR EMBL: K02011: AAA4661.1 -
 DR HIV: K02011: ENYSH8 -
 DR INTERPRO: IPR000328 -
 DR INTERPRO: IPR000777 -

FT	SIGNAL	1	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	597	851	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	BY SIMILARITY.
FT	DISULFID	119	205	BY SIMILARITY.
FT	DISULFID	126	196	BY SIMILARITY.
FT	DISULFID	131	157	BY SIMILARITY.
FT	DISULFID	228	230	BY SIMILARITY.
FT	DISULFID	228	230	BY SIMILARITY.
FT	DISULFID	286	331	BY SIMILARITY.
FT	DISULFID	378	440	BY SIMILARITY.
FT	DISULFID	385	413	BY SIMILARITY.
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	160	160	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	180	180	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	197	197	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	230	230	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	241	241	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	244	244	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	262	262	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	276	276	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	321	321	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	339	339	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	356	356	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	386	386	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	392	392	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	401	401	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	443	443	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	460	460	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	611	611	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	632	632	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	650	650	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	669	669	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	745	745	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	811	811	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	851	9664	D16A3C90857785F1 CRC64:

QY 1 ALETLLODOLLNSWCGRGRLVCTSVRRN 30
1:1 1:1:1:1:1 1:1:1:1:1 1:1 1:1
Db 577 AVERYLKDDQLLGWGCSSGLICTTAVPWN 606

ENZYME	STANDARD	PRT	852 AA.
ENZYME			
AD	12468		
DT	01-OCT-1989 (Rel. 12, Catted)		
DT	01-OCT-1989 (Rel. 12, Catted)		
DT	01-OCT-1989 (Rel. 12, last annotation update)		
DT	15-JUL-1999 (Rel. 38, last annotation update)		
DE	ENVELOPE POLYPEPTIDE GP150 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE		
DE	GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).		
GN	ENV.		
GN	Human immunodeficiency virus type 1 (HR isolate) (HY-1).		
OC	viruses: Retrof. viruses: Retroviridae: Lentivirus.		
RN	[1]		
RN	SEQUENCE FROM N. A.		
RP			
RP	MEDLINE-89083613: PubMed-2789516;		

Dandekar S.;
 RA Biological and molecular characterization of human immunodeficiency
 RT virus (HIV-1) from the brain of a patient with progressive
 RL dementia. J. Virol. 1989;63(1):1-11.
 CC -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
 CC HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
 CC -----
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 CC -----
 CC EMBL: M21098; AAA4221.1; -
 CC PIR: A21667; VCLJBR.
 CC UNIPROT: P000516; GP120.1;
 CC INTERPRO: IPR000777; -
 CC PIRAM: P000516; GP120.1;
 CC PIRAM: P000517; GP11.1;
 DR Aids; Coat protein; Glycoprotein; Transmembrane;
 KM Signal.
 FT CHAIN 1 307
 FT SIGNAL 31 507
 FT DISULFID 54 72
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 155
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 228 230
 FT DISULFID 336 435
 FT DISULFID 366 449
 FT CARBOHYD 49 45
 FT CARBOHYD 88 88
 FT CARBOHYD 135 135
 FT CARBOHYD 138 138
 FT CARBOHYD 154 154
 FT CARBOHYD 157 158
 FT CARBOHYD 178 197
 FT CARBOHYD 211 244
 FT CARBOHYD 252 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
 FT CARBOHYD 331 331
 FT CARBOHYD 334 324
 FT CARBOHYD 384 384
 FT CARBOHYD 390 390
 FT CARBOHYD 396 396
 FT CARBOHYD 400 400
 FT CARBOHYD 442 442
 FT CARBOHYD 456 456
 FT CARBOHYD 607 607
 FT CARBOHYD 632 632
 FT CARBOHYD 633 633
 FT CARBOHYD 670 670
 FT CARBOHYD 812 812
 FT SEQUENCE 852 AA: 97203 MW: 28866345DE9C915F CRC64;
 Query Match 56.0%; Score 102; DB 1; Length 852;
 Best Local Similarity 56.7%;
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Oy 1 ALETHLONGLINSGRCGRVLCVTSYRN 30
 DB 578 AVEHYKDDQLGIGGSCSKLCTIVAHN 607
 RESULT 9
 ENV_HV153 STANDARD: PRT: 852 AA.
 AC P19549:1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
 DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 RN SOURCE FROM N.A.
 RX MEDLINE-90317906; PubMed-2370688;
 RA York-Higgins D., Cheng-Meyer C., Bauer D., Levy J.A., Dina D.;
 RT "Human immunodeficiency virus type 1 cellular host range, of
 RT the viral genome".
 RL J. Virol. 64:4016-4020(1990).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M38427; AAA5067.1; -
 CC UNIPROT: P000516; GP120.1;
 CC INTERPRO: IPR000777; -
 CC PIRAM: P000516; GP120.1;
 CC PIRAM: P000517; GP11.1;
 DR Aids; Coat protein; Glycoprotein; Transmembrane;
 KM Signal.
 FT CHAIN 1 29
 FT SIGNAL 30 507
 FT DISULFID 53 76
 FT DISULFID 118 203
 FT DISULFID 125 197
 FT DISULFID 130 156
 FT DISULFID 219 248
 FT DISULFID 229 240
 FT DISULFID 337 433
 FT DISULFID 384 412
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 142 142
 FT CARBOHYD 152 152
 FT CARBOHYD 155 155
 FT CARBOHYD 189 189
 FT CARBOHYD 198 198
 FT CARBOHYD 242 242
 FT CARBOHYD 263 263
 FT CARBOHYD 277 277
 FT CARBOHYD 290 290
 FT CARBOHYD 296 296
 FT CARBOHYD 326 326
 FT CARBOHYD 332 332
 FT CARBOHYD 355 355
 FT CARBOHYD 385 385
 FT CARBOHYD 391 391
 FT SEQUENCE 852 AA: 97203 MW: 28866345DE9C915F CRC64;
 Query Match 56.0%; Score 102; DB 1; Length 852;
 Best Local Similarity 56.7%;
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Query Match 58.0%; Score 102; DB 1; Length 852;
 Best Local Similarity 56.7%; Pred. No. 3, 6e-07;
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

1 AETLLDNOQLLNSGCCRGRLVCTYSYRNN 30
 578 AVERLADQQLGLMGCSKRLICTIVPWN 607

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 852 AA; 96663 MW; BE7BHB023C9910D CRC64;

Query Match 58.0%; Score 102; DB 1; Length 852;
 Best Local Similarity 56.7%; Pred. No. 3, 6e-07;
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

1 AETLLDNOQLLNSGCCRGRLVCTYSYRNN 30
 578 AVERLADQQLGLMGCSKRLICTIVPWN 607

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 852 AA; 96663 MW; BE7BHB023C9910D CRC64;

RESULT 10
 ID ENV_HV1A2 STANDARD: PRT: 853 AA.
 AC P19551;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DE 15-JUL-1998 (Rel. 38, Last annotation update)
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
 GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
 ENV.
 CC Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
 CC Viruses; Retroviridae; Lentiviridae; Lentivirus.
 CC [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:90317877; PubMed:1695254;
 RA Stevenson M., Haggerty S., Lamont C., Mann A.M., Weiser C.,
 RA Wasik A.;
 CC "Cloning and characterization of human immunodeficiency virus type 1
 variants diminished in the ability to induce syncytium-independent
 cytolysis." J. VIOL. 64:3792-3803(1990).
 CC 3. VIOL. 64:3792-3803(1990).
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 or send an email to license@isb-sib.ch).
 CC EMBL: M31943; .
 CC HIV: M31943; ENV582.1;
 DR INTERPRO: IPR000328;
 DR INTERPRO: IPR000772;
 DR PFAM: PF00516; GP120. 1.
 DR PFAM: PF00517; GP41. 1.
 KM AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 RM Signal.
 FT SIGNAL 1 30
 FT CHAIN 510 853 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 119 203 BY SIMILARITY.
 FT DISULFID 126 194 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 216 245 BY SIMILARITY.
 FT DISULFID 226 237 BY SIMILARITY.
 FT DISULFID 274 329 BY SIMILARITY.
 FT DISULFID 303 416 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 58.0%; Score 102; DB 1; Length 853;
 Best Local Similarity 56.7%; Pred. No. 3, 7e-07;
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

1 AETLLDNOQLLNSGCCRGRLVCTYSYRNN 30
 580 AVERLADQQLGLMGCSKRLICTIVPWN 609

FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 712 712 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 853 AA; 96912 MW; 3377B93B6F22A8A CRC64;

Query Match 58.0%; Score 102; DB 1; Length 853;
 Best Local Similarity 56.7%; Pred. No. 3, 7e-07;
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

1 AETLLDNOQLLNSGCCRGRLVCTYSYRNN 30
 580 AVERLADQQLGLMGCSKRLICTIVPWN 609

FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 712 712 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 853 AA; 96912 MW; 3377B93B6F22A8A CRC64;

RESULT 11
 ID ENV_HV1A2 STANDARD: PRT: 855 AA.
 AC P03378;
 DT 01-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 38, Last annotation update)
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
 GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
 ENV.
 CC Human immunodeficiency virus type 1 (AIV/SF2 isolate) (HIV-1).
 CC Viruses; Retroviridae; Lentiviridae; Lentivirus.
 CC [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:8500453; PubMed:2578227;
 RA Stamenkovic I., Brown-Schuler S.L., Gee W.W., Renard A., Randoiph A.,
 RA Levy J.A., Dits D., Lucif P.A.;
 CC "Nucleotide sequence and expression of an AIDS-associated retrovirus
 (AIV-2)." Science 227:484-492(1985).
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 or send an email to license@isb-sib.ch).
 CC EMBL: X02807; AA859882.1;
 DR PIR: A03976; VCL2A2.
 DR HIV: K02007; ENV582.1;

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DR INTERPRO: IP000328; -
DR INTERPRO: IP000777; -
DR PFM: PF00516; GP120; 1.
DR AID5: Coat protein: Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CARBOHYD 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 208
FT DISULFID 125 199
FT DISULFID 130 155
FT DISULFID 221 250
FT DISULFID 231 242
FT DISULFID 321 335
FT DISULFID 387 415
FT DISULFID 387 415
FT CARBOHYD 87 129
FT CARBOHYD 129 129
FT CARBOHYD 140 140
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 184 184
FT CARBOHYD 190 190
FT CARBOHYD 233 233
FT CARBOHYD 244 244
FT CARBOHYD 265 265
FT CARBOHYD 279 279
FT CARBOHYD 292 292
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FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 815 815
SEQUENCE 855 AA; 97438 MW; A39C2057AAC1A2 CRC64;

FT SIGNAL 1 30
FT CARBOHYD 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 208
FT DISULFID 125 199
FT DISULFID 130 155
FT DISULFID 221 250
FT DISULFID 231 242
FT DISULFID 321 335
FT DISULFID 387 415
FT DISULFID 387 415
FT CARBOHYD 87 129
FT CARBOHYD 129 129
FT CARBOHYD 140 140
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 184 184
FT CARBOHYD 190 190
FT CARBOHYD 233 233
FT CARBOHYD 244 244
FT CARBOHYD 265 265
FT CARBOHYD 279 279
FT CARBOHYD 292 292
FT CARBOHYD 298 298
FT CARBOHYD 304 304
FT CARBOHYD 324 324
FT CARBOHYD 354 354
FT CARBOHYD 364 364
FT CARBOHYD 388 388
FT CARBOHYD 394 394
FT CARBOHYD 400 400
FT CARBOHYD 408 408
FT CARBOHYD 445 445
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FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 815 815
SEQUENCE 855 AA; 97438 MW; A39C2057AAC1A2 CRC64;

Query Match 58.0%; Score 102; DB 1; Length 855;
Best Local Similarity 56.7%; Pred. No. 3,7e-07;
Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 ALETLIQNOLLNSWCGRLVCYTSVMN 30
DB 581 AVERYLRDQDLGICWGSCKRLTCTAVPMN 510

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RN SEQUENCE FROM N.A.
RX MEDLINE-0014544; Pubmed-2859749;
RA Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.;
RT "A highly defective HIV-1 strain isolated from a healthy gabonese
individual presenting an atypical western blot.":
AIDS 3:707-715(1989).
RL MISCELLANEOUS: THE OTI ISOLATE WAS TAKEN FROM THE BLOOD OF A
CC -HIV-1 POSITIVE INDIVIDUAL.
CC -----
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CC modified and this statement is not removed. Usage by for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M26727; AA81397.1; -
DR HIV: M26727; ENV50Y1.
DR INTERPRO: IP000328; -
DR INTERPRO: IP000777; -
DR PFM: PF00516; GP120; 1.
DR AID5: Coat protein: Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CARBOHYD 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 321 335
FT DISULFID 381 415
FT DISULFID 388 415
FT CARBOHYD 87 134
FT CARBOHYD 134 134
FT CARBOHYD 142 142
FT CARBOHYD 145 145
FT CARBOHYD 161 161
FT CARBOHYD 165 165
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FT CARBOHYD 815 815
SEQUENCE 855 AA; 97476 MW; 9CF82A07ADD62DA CRC64;

Query Match 58.0%; Score 102; DB 1; Length 855;
Best Local Similarity 56.7%; Pred. No. 3,7e-07;
Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 ALETLIQNOLLNSWCGRLVCYTSVMN 30

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Db 581 AVERYKID00LLGIMCSGSKLICTTVPNN 610

RESULT 13

ENV_HYB1H1 STANDARD: PRT: 856 AA.

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
NM Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
PP Sequence from N.A.
RX MEDLINE-85111123; PubMed-2578615.
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starich B.R.,
Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
Baumsteier K., Ivanoff L., Peltway S.R.J., Pearson M.L.,
Lautenberger J.A., Papas T.S., Chirayab J., Chang N.T., Gallo R.C.,
Wong-Staal F.,
RT Complete nucleotide sequence of the AIDS virus, HTLV-III.
RM Nucleotide 513:277-284(1985).

DISULFIDE BONDS, AND CARBOHYDRATE LINKAGE SITES.

MEDLINE-90285159; PubMed-2355006.

RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
Gregory T.J.

RT Assignment of intrachain disulfide bonds and characterization of
potential glycosylation sites of the type 1 recombinant human
immunodeficiency virus envelope glycoprotein (gp120) expressed in
Chinese hamster ovary cells (115382,11990).

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).

EMBL: M15654; AAA4205.1; -

PIR: A03973; VCLH3.

HIV: M15654; ENVBHI02.

INTERNO: IPR000328; -

PERNO: IPR000777; -

PEAK: P00516; GP120.1.

ATIR: P00517; GP41.1.

CC Code Protein: Polypeptide; Glycoprotein; Transmembrane;

SIGNAL.

FT CHAIN 1 30

FT CHAIN 512 856

FT DISULFID 54 74

FT DISULFID 119 205

FT DISULFID 126 196

FT DISULFID 214 217

FT DISULFID 228 239

FT DISULFID 296 331

FT DISULFID 378 445

FT DISULFID 385 418

FT CARBOHYD 88 88

FT CARBOHYD 136 136

FT CARBOHYD 141 141

FT CARBOHYD 158 158

FT CARBOHYD 186 186

FT CARBOHYD 197 197

EXTERIOR MEMBRANE GLYCOPROTEIN.

TRANSMEMBRANE GLYCOPROTEIN.

FT CARBOHYD 230 230 N-LINKED (GLCNAc...)
FT CARBOHYD 234 241 N-LINKED (GLCNAc...)
FT CARBOHYD 241 241 N-LINKED (GLCNAc...)
FT CARBOHYD 262 262 N-LINKED (GLCNAc...)
FT CARBOHYD 276 276 N-LINKED (GLCNAc...)
FT CARBOHYD 289 289 N-LINKED (GLCNAc...)
FT CARBOHYD 295 295 N-LINKED (GLCNAc...)
FT CARBOHYD 301 301 N-LINKED (GLCNAc...)
FT CARBOHYD 332 332 N-LINKED (GLCNAc...)
FT CARBOHYD 332 332 N-LINKED (GLCNAc...)
FT CARBOHYD 352 352 N-LINKED (GLCNAc...)
FT CARBOHYD 386 386 N-LINKED (GLCNAc...)
FT CARBOHYD 392 392 N-LINKED (GLCNAc...)
FT CARBOHYD 397 397 N-LINKED (GLCNAc...)
FT CARBOHYD 406 406 N-LINKED (GLCNAc...)
FT CARBOHYD 448 448 N-LINKED (GLCNAc...)
FT CARBOHYD 463 463 N-LINKED (GLCNAc...)
FT CARBOHYD 611 611 N-LINKED (GLCNAc...)
FT CARBOHYD 616 616 N-LINKED (GLCNAc...)
FT CARBOHYD 637 637 N-LINKED (GLCNAc...)
FT CARBOHYD 674 674 N-LINKED (GLCNAc...)
FT CARBOHYD 750 750 N-LINKED (GLCNAc...)
FT CARBOHYD 816 816 N-LINKED (GLCNAc...)
SO SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931B27 CRC64;

Query Match 58.0%; Score 102; DB 1; Length 856;
Nucleic Acid Similarity 56.7%; Pred. No. 3.7e-07;
Matches 17; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY 1 ALETTLOOOLLGIMCSGSKLICTTVPNN 30
DB 582 AVERYKID00LLGIMCSGSKLICTTVPNN 611

RESULT 14

ENV_HYB1H2 STANDARD: PRT: 856 AA.

AC P04578; 009779; -

DT 13-AUG-1987 (Rel. 05, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE

GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].

GN ENV.

NM Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

PP Sequence from N.A.

RX MEDLINE-87299196; PubMed-3040055;

RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,

Gallo R.C., Wong-Staal F.

RT Complete nucleotide sequences of functional clones of the AIDS

virus, HTLV-III, and HTLV-IIIb.

RM AIDS Res. Hum. Retroviruses 3:57-69(1987).

CC Code Protein: Polypeptide; Glycoprotein; Transmembrane;

SIGNAL.

FT CHAIN 1 30

FT CHAIN 512 856

FT DISULFID 54 74

FT DISULFID 119 205

FT DISULFID 126 196

FT DISULFID 214 217

FT DISULFID 228 239

FT DISULFID 296 331

FT DISULFID 378 445

FT DISULFID 385 418

FT CARBOHYD 88 88

FT CARBOHYD 136 136

FT CARBOHYD 141 141

FT CARBOHYD 158 158

FT CARBOHYD 186 186

FT CARBOHYD 197 197

Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.

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or send an email to license@sib-sib.ch).

EMBL: K03455; AA050262.1; -

EMBL: AF038399; AA099976.1; -

EMBL: AF038399; AA099976.1; -

EMBL: AF038399; AA099976.1; -

EMBL: AF038399; AA099976.1; -

EMBL: AF038399; AA099976.1; -

Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

```

Qy      1 ALETTLQNOOLNSMGCGRGLVCYTSVRWN 30
          | : | : | : | : | : | : | : |
Db      582 AVERYLKDQQLGIMGSGKLICTTAVPWN 611

```

Search completed: March 22, 2001, 09:57:50
Job time: 425 sec

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Db 584 ALETLQNDQNLISWCGRGRLVCTYSVKNMT 615

RESULT 3

S21902
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 19-Mar-1997 #sequence_rev150n 24-Jul-1997 #text_change 26-Aug-1999
C:Accession: S49197
R:Chanseau, P.; Borman, A.M.; Quillent, C.; Gueard, D.; Chamaret, S.; Cohen, J.; Remy, submitted to the EMBL Data Library, July 1994
A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defi
A:Reference number: S49197
A:Molecule type: RNA
A:Residues: 1-877 <CHAS>
A:Cross-references: EMBL:X80020; NID:9510516; PIDN:CAA5623.1; PID:9510517
C:Experimental source: isolate VAV
C:Superfamily: type E retrovirus env polyprotein
Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein
P:1-335/Product: signal sequence status predicted <SIG>
P:1-335/Product: coat protein gp120 status predicted <CP1>
P:698-716/Product: transmembrane status predicted <TM>
P:59-88,139,146,155,184,189,190,230,253,242,263,270,277,292,302,333,345,357,367,396,404,

Query Match 85.5%; Score 147; DB 2; Length 877;
Best Local Similarity 75.0%; Pred. No. 9,3e-13;

Matches 24; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 597 ALETFQNDQNLISWCGRGRLVCTYSVKNMT 628

RESULT 4

VCLST
env polyprotein precursor - simian immunodeficiency virus SIVcpz
M:Domain: gp120; coat protein gp41
C:Species: simian immunodeficiency virus
C:Accession: S09990
C>Date: 30-Sep-1991 #sequence_rev150n 30-Sep-1991 #text_change 16-Jul-1999
R:Huet, T.; Chevillier, R.; Meyers, A.; Roelants, G.; Wahl-Jobson, S.
Nature 345, 356-359, 1990
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
Accession: S09990
A:Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36407.1; PID:958874

A:Residues: 1-854 <HUE>
A:Molecule type: DNA
A:Status: nucleic acid sequence not shown; translation not shown
C:Genetics:
A:Genes: env
C:Superfamily: type E retrovirus env polyprotein
C:Experimental source: isolate VAV
P:1-30/Domain: signal sequence status predicted <SIG>
P:31-500/Product: coat protein gp120 status predicted <CP1>
P:501-854/Product: coat protein gp41 status predicted <CP2>
P:675-693/Domain: transmembrane status predicted <TM>
P:805-821/Domain: transmembrane status predicted <TM>
P:134,140,143,154,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45

Query Match 62.5%; Score 110; DB 1; Length 854;
Best Local Similarity 56.2%; Pred. No. 1,4e-07;
Matches 18; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Db 1 ALETLQNDQNLISWCGRGRLVCTYSVKNMT 32

Db 572 AVERYLDQDLISWCGRGRLVCTYVPMN 603

RESULT 5

S21902
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_rev150n 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S21902
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W. submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete
A:Reference number: S21902
A:Accession: S21902
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STES>
A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA3626.1; PID:960176
C:Superfamily: type E retrovirus env polyprotein

Query Match 59.7%; Score 105; DB 2; Length 357;
Best Local Similarity 60.0%; Pred. No. 3,1e-07;

Matches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 83 AVERYLDQDLISWCGRGRLVCTYVPMN 112

RESULT 6

S70423
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 20) (frag
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 20
C:Accession: S70423
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; NID:92144209
A:Accession: S70423
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STES>
A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA3626.1; PID:960176
C:Superfamily: type E retrovirus env polyprotein

Query Match 59.7%; Score 105; DB 2; Length 357;
Best Local Similarity 60.0%; Pred. No. 3,1e-07;
Matches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 83 AVERYLDQDLISWCGRGRLVCTYVPMN 112

RESULT 7

S22002
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_rev150n 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S22002
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W. submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete
A:Reference number: S22002
A:Accession: S22002
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STES>

Query Match 59.7%; Score 105; DB 2; Length 357;
Best Local Similarity 60.0%; Pred. No. 3,1e-07;
Matches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 83 AVERYLDQDLISWCGRGRLVCTYVPMN 112

C:Superfamily: type E retrovirus env polyprotein

Query Match 59.7%; Score 105; DB 2; Length 358;

Best Local Similarity 60.0%; Pred. No. 3.1e-07; Mismatches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

1 ALETLNQQGLNSGCRGRVCTSVNPN 30

DB 84 AVERLKNQQLGIMGCSRLICTTAVNPN 113

RESULT 8
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 31), (fragment

C:Species: human immunodeficiency virus type 1, HIV-1

C:Accession: S70418 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb

A:Reference number: S70417; MUID:92144209

A:Accession: S70418

A:Status: preliminary

A:Molecule type: RNA

A:Cross-references: EMBL:X61357

C:Superfamily: type E retrovirus env polyprotein

Query Match 59.7%; Score 105; DB 2; Length 358;

Best Local Similarity 60.0%; Pred. No. 3.1e-07; Mismatches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

1 ALETLNQQGLNSGCRGRVCTSVNPN 30

DB 84 AVERLKNQQLGIMGCSRLICTTAVNPN 113

RESULT 9
env polyprotein D - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polyprotein gp41; carboxyl end of coat protein gp120

M:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

A:Note: host Homo sapiens (man)

C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 31-Jan-1997

Accession: B41621

Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A:Reference number: A41621; MUID:92107924

A:Accession: B41621

A:Molecule type: RNA

A:Cross-references: GB:M77279

A:Note: This virus was isolated from the daughter

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F:434/Protein: coat protein gp120 (fragment); status predicted <GR2>

F:435-454/Domain: transmembrane status predicted <RM>

F:9,23,36,42,48,49,78,85,102,108,132,138,142,155,210,214,362,367,376/Binding site: carbo

DB 333 ALETLNQQGLNSGCRGRVCTSVNPN 362

RESULT 10
envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Accession: S72000 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL data library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S22000

A:Status: preliminary

A:Molecule type: RNA

A:Cross-references: EMBL:X61351

C:Superfamily: type E retrovirus env polyprotein

Query Match 59.1%; Score 104; DB 2; Length 358;

Best Local Similarity 60.0%; Pred. No. 4.3e-07; Mismatches 18; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

1 ALETLNQQGLNSGCRGRVCTSVNPN 30

DB 84 AVERLKNQQLGIMGCSRLICTTAVNPN 113

RESULT 11
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3b) (fragm

C:Species: human immunodeficiency virus type 1, HIV-1

C:Accession: S70417 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209

A:Accession: S70417

A:Status: preliminary

A:Molecule type: RNA

A:Cross-references: EMBL:X61351

C:Superfamily: type E retrovirus env polyprotein

Query Match 59.1%; Score 104; DB 2; Length 358;

Best Local Similarity 60.0%; Pred. No. 4.3e-07; Mismatches 18; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

1 ALETLNQQGLNSGCRGRVCTSVNPN 30

DB 84 AVERLKNQQLGIMGCSRLICTTAVNPN 113

RESULT 12
env polyprotein P - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polyprotein gp41; carboxyl end of coat protein gp120

M:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

A:Note: host Homo sapiens (man)

C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999

Accession: C41621

Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversit

A:Reference number: A41621; MUID:92107924

A:Accession: C41621

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 22, 2001, 10:00:46 ; Search time 171.82 Seconds

(Without alignments)
21.823 Million cell updates/sec

Title: US-09-147-362-12

Sequence: 1 ALETLNQQILNIMCGRILCYTVRNNEI 32

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Maximum number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

1: SP_RPMEL.15:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_Other:*
8: SP_Protistelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*

Pred. NO. is the number of results predicted by chance to have a
score at least as high as the observed score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165	93.8	126	12	091HUV
2	165	93.8	126	12	091HUV
3	165	93.8	126	12	091EB3
4	165	93.8	126	12	091EB3
5	164	93.2	240	12	091EC2
6	163	92.6	125	12	091H08
7	163	92.6	125	12	091EA5
8	163	92.6	125	12	091EB9
9	162	92.0	115	12	091HVS
10	162	92.0	115	12	091HVS
11	162	92.0	208	12	091EA3
12	162	92.0	216	12	091EC5
13	162	92.0	342	12	011942
14	162	92.0	418	12	036547
15	162	92.0	871	12	057074
16	161	91.5	105	12	011939
17	161	91.5	114	12	040452
18	161	91.5	114	12	040452
19	161	91.5	213	12	091EC4

20	161	91.5	512	12	091EP0	091ef0 human immun
21	160	90.9	116	12	040458	040458 human immun
22	160	90.9	134	12	091HVA	091hva human immun
23	160	90.9	183	12	091EC1	091ec1 human immun
24	160	90.9	209	12	091E66	091e66 human immun
25	160	90.9	220	12	091EC9	091ec9 human immun
26	160	90.9	225	12	091EA0	091ea0 human immun
27	160	90.9	512	12	091EB2	091eb2 human immun
28	160	90.9	517	12	091EB2	091eb2 human immun
29	160	90.9	875	12	091HVS	091hvs human immun
30	160	90.9	900	12	090N28	090n28 human immun
31	159	90.3	104	12	076153	076163 human immun
32	159	90.3	114	12	040457	040457 human immun
33	159	90.3	200	12	091EB8	091eb8 human immun
34	159	90.3	224	12	091EA8	091ea8 human immun
35	159	90.3	230	12	091EB2	091eb2 human immun
36	159	90.3	517	12	091EB2	091eb2 human immun
37	158	89.8	111	12	040453	040453 human immun
38	158	89.8	133	12	091HVS	091hvs human immun
39	158	89.8	177	12	091EB0	091eb0 human immun
40	158	89.8	232	12	091EB6	091eb6 human immun
41	158	89.8	242	12	091E30	091e30 human immun
42	158	89.8	243	12	091E35	091e35 human immun
43	158	89.8	502	12	091E33	091e33 human immun
44	158	89.8	114	12	040448	040448 human immun
45	157	89.2				

ALIGNMENTS

RESULT 1

091HUV PRELIMINARY; PRT; 124 AA.
ID 091HUV;
AC 091HUV; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
GN ENVELOPE GLYCOPROTEIN (FRAGMENT).
OS GP41.
OC Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
NC NCB1_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang C., Gao F., Fontjorge P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lai R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O.";
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL: AF229237; AAF71914.1; -;
FT NON-ITER
FT NON-ITER
SQ SEQUENCE 124 AA; 15187 MW; 105D515F14450F8 CRC64;

Query Match 93.8%; Score 165; DB 12; Length 124;

Best Local Similarity 84.4%; Pred. No. 2,7e-17;

Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 23 ALETLNQQILNIMCGRILCYTVRNNEI 32

1 ALETLNQQILNIMCGRILCYTVRNNEI 32

1 ALETLNQQILNIMCGRILCYTVRNNEI 32

1 ALETLNQQILNIMCGRILCYTVRNNEI 32

1 ALETLNQQILNIMCGRILCYTVRNNEI 32

1 ALETLNQQILNIMCGRILCYTVRNNEI 32

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN GP41.
 OS Human Immunodeficiency virus type 1.
 RC Retrovirda: Retroviridae; Lentivirus.
 NCBI_TaxID=11676;
 RN 11
 RA SEQUENCE FROM N.A.
 RC STRAIN=97H300;
 RA Yang C., Cao F., Fonjuno P.N., Zekeng L., van der Groen G.,
 RA Platenazek D., Schable C., Lal R.B.;
 RT Phylogenetic analysis of protease and transmembrane regions of HIV
 RT type 1 group O.*;
 DR AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
 FT NON-TER
 SO SEQUENCE 126 AA: 15169 MW: 13501BDCCF0DD CRC64;

Query Match 93.8%; Score 165; DB 12; Length 126;
 Best local Similarity 87.5%; Pred.No. 2.8e-17;
 Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

1 ALETLQNDLQNLIMGCRGLVCTSYVMNMT 32
 Db 30 ALETLQNDLQNLIMGCRGLVCTSYVMNMTS 61

RESULT 3
 ID 091E83 PRELIMINARY: PRT: 172 AA.
 AC 091E83
 DT 01-OCT-2000 (TREMBlrel. 15. Created)
 DT 01-OCT-2000 (TREMBlrel. 15. Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15. Last annotation update)
 DE GP41 (FRAGMENT).
 GN ENV.
 OS Human Immunodeficiency virus type 1.
 OC Viruses; Retrovirda: Retroviridae; Lentivirus.
 NCBI_TaxID=11676;
 RN 11
 RA SEQUENCE FROM N.A.
 RC STRAIN=BCF99;
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 RT Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.*;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ236407; CAB96255.1;
 FT NON-TER
 SO SEQUENCE 172 AA: 20388 MW: 972C7AF2A7546B13 CRC64;

Query Match 93.8%; Score 165; DB 12; Length 172;
 Best local Similarity 84.4%; Pred.No. 3.7e-17;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

1 ALETLQNDLQNLIMGCRGLVCTSYVMNMT 32
 Db 26 ALETLQNDLQNLIMGCRGLVCTSYVMNMT 57

RESULT 4
 ID 091E82 PRELIMINARY: PRT: 234 AA.
 AC 091E82
 DT 01-OCT-2000 (TREMBlrel. 15. Created)
 DT 01-OCT-2000 (TREMBlrel. 15. Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15. Last annotation update)
 DE GP41 (FRAGMENT).
 GN ENV.
 OS Human Immunodeficiency virus type 1.
 OC Viruses; Retrovirda: Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
 RN 11
 RA SEQUENCE FROM N.A.
 RC STRAIN=BCF100;
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 RT Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.*;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ236397; CAB96246.1;
 FT NON-TER
 SO SEQUENCE 234 AA: 27036 MW: 399050J38555A8C CRC64;

Query Match 93.8%; Score 165; DB 12; Length 234;
 Best local Similarity 84.4%; Pred.No. 5e-17;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

1 ALETLQNDLQNLIMGCRGLVCTSYVMNMT 32
 Db 48 ALETLQNDLQNLIMGCRGLVCTSYVMNMT 79

RESULT 5
 ID 091E32 PRELIMINARY: PRT: 240 AA.
 AC 091E32
 DT 01-OCT-2000 (TREMBlrel. 15. Created)
 DT 01-OCT-2000 (TREMBlrel. 15. Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15. Last annotation update)
 DE TM, GP41 (FRAGMENT).
 GN ENV.
 OS Human Immunodeficiency virus type 1.
 OC Viruses; Retrovirda: Retroviridae; Lentivirus.
 NCBI_TaxID=11676;
 RN 11
 RA SEQUENCE FROM N.A.
 RC STRAIN=BCF11;
 RA Deplenne C., Brun-Vezinet F., Dormont D., Simon F.O.;
 RT Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates.*;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ243365; CAB96335.1;
 FT NON-TER
 SO SEQUENCE 240 AA: 27723 MW: 1E206E8D91A197 CRC64;

Query Match 93.2%; Score 164; DB 12; Length 240;
 Best local Similarity 84.4%; Pred.No. 7.3e-17;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

1 ALETLQNDLQNLIMGCRGLVCTSYVMNMT 32
 Db 50 ALETLQNDLQNLIMGCRGLVCTSYVMNMT 81

RESULT 6
 ID 091H08 PRELIMINARY: PRT: 135 AA.
 AC 091H08
 DT 01-OCT-2000 (TREMBlrel. 15. Created)
 DT 01-OCT-2000 (TREMBlrel. 15. Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15. Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN GP41.
 OS Human Immunodeficiency virus type 1.
 OC Viruses; Retrovirda: Retroviridae; Lentivirus.
 NCBI_TaxID=11676;
 RN 11
 RA SEQUENCE FROM N.A.
 RC STRAIN=97HC76;
 RA Yang C., Cao F., Fonjuno P.N., Zekeng L., van der Groen G.,

Fri Mar 23 07:47:33 2001

RA Pieniazek D., Schable C., Lal R.B.:
 "Phylogenetic analysis of protease and transmembrane regions of HIV
 type 1 group O."
 RT AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
 RL EMBL: AF229236; AAF71913.1; "

DR EMBL: AF229236; AAF71913.1; "
 FT NON_TER 125 125
 FT NON_TER 125 125
 SO SEQUENCE 125 AA; 15108 MW; EA2896CA25FEF342 CRC64;

Query Match
 Best Local Similarity 81.2%; Pred. No. 5,5e-17;
 Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLINMGCRGLVCTSVNNMT 32
 DB 27 ALETLIONOOLLINMGCRGLVCTSVNNMT 58

RESULT 7
 ID 091EAS PRELIMINARY; PRT: 216 AA.

AC 091EAS;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE GP41 (FRAGMENT).

OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;

RA SEQUENCE FROM N.A.
 RC STRAIN=JEF26;
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 Philippe M.;
 RT Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates. "

DR EMBL: AJ226415; CAB96263.1; "
 FT NON_TER 216 216
 FT NON_TER 216 216
 SO SEQUENCE 216 AA; 25003 MW; 0A5AC218BFA8932 CRC64;

Query Match
 Best Local Similarity 82.6%; Score 163; DB 13; Length 216;
 Pred. No. 9,3e-11;
 Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLINMGCRGLVCTSVNNMT 32
 DB 32 ALETLIONOOLLINMGCRGLVCTSVNNMT 63

RESULT 8
 ID 091ED9 PRELIMINARY; PRT: 544 AA.

AC 091ED9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ENV POLYPEPTIDE (FRAGMENT).

OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;

RA SEQUENCE FROM N.A.
 RC STRAIN=YF26;
 RA Roques P., Robertson D., Diamond F., Soussignere S., Mauchere F.,
 Depienne C., Brun-Vezinet F., Dornmont D.;
 RT HIV-1 group O phylogenetic analysis of C2-gp41 region. "

DR EMBL: AF229236; AAF71913.1; "
 FT NON_TER 137 137
 FT NON_TER 137 137
 SO SEQUENCE 137 AA; 16494 MW; 55CA7096D8168493 CRC64;

FT NON_TER 1 1
 FT NON_TER 544 544
 SO SEQUENCE 544 AA; 61398 MW; FC3CFME31DB6D50 CRC64;

Query Match
 Best Local Similarity 87.5%; Pred. No. 2,3e-16;
 Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLINMGCRGLVCTSVNNMT 32
 DB 360 ALETLIONOOLLINMGCRGLVCTSVNNMT 391

RESULT 9
 ID 0A0450 PRELIMINARY; PRT: 116 AA.

AC 0A0450;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).

OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;

RA SEQUENCE FROM N.A.
 RC STRAIN=Group O.
 RA Bitollet-Buchle F., Ekasa E., Peeters M., Delaporte E.;
 RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL: Y09775; CA70914.1; "

DR INTERPRO: IPR000328; "
 DR PFM: PFM00517; GP41; 1;
 FT NON_TER 116 116
 FT NON_TER 116 116
 SO SEQUENCE 116 AA; 13975 MW; 12B3D0DDDA1AD32 CRC64;

Query Match
 Best Local Similarity 92.0%; Score 162; DB 12; Length 116;
 Pred. No. 7,2e-17;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLINMGCRGLVCTSVNNMT 32
 DB 29 ALETLIONOOLLINMGCRGLVCTSVNNMT 60

RESULT 10
 ID 091HVS PRELIMINARY; PRT: 137 AA.

AC 091HVS;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;

RA SEQUENCE FROM N.A.
 RC STRAIN=97CWT61;
 RA Yang C., Gao F., Fontjuno P.N., Zekeng L., van der Groen G.,
 Pieniazek D., Schable C., Lal R.B.;
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV
 type 1 group O."

RT AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
 DR EMBL: AF229236; AAF71913.1; "
 FT NON_TER 137 137
 FT NON_TER 137 137
 SO SEQUENCE 137 AA; 16494 MW; 55CA7096D8168493 CRC64;

Query Match 92.0%; Score 162; DB 12; Length 137;
 Best Local Similarity 84.4%; Pred. No. 8,4e-17;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLQNDQNLIMGCRGLVCTSVNNET 32
 DB 30 ALETLQNDQNLIMGCRGLVCTSVNNET 61

RESULT 11

ID 091EA3 PRELIMINARY; PRT; 208 AA.

AC 091EA3-2000 (TREMBLER, 15, Created)
 DT 01-OCT-2000 (TREMBLER, 15, Last sequence update)
 DE 01-OCT-2000 (TREMBLER, 15, Last annotation update)
 GN GP41 (FRAGMENT).
 ENV. Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;
 RA NCBI

RC STRAIN=VAF32;
 RD SEQUENCE FROM N.A.

RA Philippe M.; Robertson D., Sandrine S., Christel D., Francois S.,
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ26417; CAB96285.1;

DR NON_TER 208
 FT NON_TER 1
 SQ SEQUENCE 208 AA; 24286 MW; 1C2961C1953A07A1 CRC64;

Query Match 92.0%; Score 162; DB 12; Length 208;
 Best Local Similarity 81.2%; Pred. No. 1,3e-16;
 Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLQNDQNLIMGCRGLVCTSVNNET 32
 DB 24 ALETLQNDQNLIMGCRGLVCTSVNNET 55

RESULT 12

ID 091EC5 PRELIMINARY; PRT; 216 AA.

AC 091EC5-2000 (TREMBLER, 15, Created)
 DT 01-OCT-2000 (TREMBLER, 15, Last sequence update)
 DE 01-OCT-2000 (TREMBLER, 15, Last annotation update)
 GN GP41 (FRAGMENT).
 ENV. Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;
 RA NCBI

RC STRAIN=BCF07;
 RD SEQUENCE FROM N.A.

RA Philippe M.; Robertson D., Sandrine S., Christel D., Francois S.,
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ26394; CAB96443.1;

DR NON_TER 216
 FT NON_TER 1
 SQ SEQUENCE 216 AA; 25027 MW; 413AE9BFB4FC9A CRC64;

Query Match 92.0%; Score 162; DB 12; Length 216;
 Best Local Similarity 87.5%; Pred. No. 1,3e-16;
 Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLQNDQNLIMGCRGLVCTSVNNET 32
 DB 37 ALETLQNDQNLIMGCRGLVCTSVNNET 68

RESULT 13

ID 011942 PRELIMINARY; PRT; 342 AA.

AC 011942-1997 (TREMBLER, 04, Created)
 DT 01-JUL-1997 (TREMBLER, 04, Last sequence update)
 DE 01-MAY-2000 (TREMBLER, 13, Last annotation update)
 GN ENVELOPE GLYCOPROTEIN (FRAGMENT).
 ENV. Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;
 RA NCBI

RC STRAIN=AF21561;
 RD SEQUENCE FROM N.A.

RA Medicine-97340911; PubMed-9197385;
 RX Hickman R.K., Gurtler L., Kaplue L., von Overbeck J., Hampel H.,
 RA Devare S.G.,
 RA "Sequence of gp120, a major immunodominant region of HIV type 1 group O from
 RT West central Africa."

RT "Sequence of gp120, a major immunodominant region of HIV type 1 group O from
 RT West central Africa."

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF21561.1;

DR INTERPRO: IPR000328;
 DR PFM: PFM0517; GP41.1;

KW Envelope protein.
 FT NON_TER 342
 SQ SEQUENCE 342 AA; 38464 MW; E337FECBA23B67A1 CRC64;

Query Match 92.0%; Score 162; DB 12; Length 342;
 Best Local Similarity 84.4%; Pred. No. 2,1e-16;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLQNDQNLIMGCRGLVCTSVNNET 32
 DB 65 ALETLQNDQNLIMGCRGLVCTSVNNET 96

RESULT 14

ID 036547 PRELIMINARY; PRT; 418 AA.

AC 036547-1998 (TREMBLER, 05, Created)
 DT 01-JAN-1998 (TREMBLER, 05, Last sequence update)
 DE 01-MAY-2000 (TREMBLER, 13, Last annotation update)
 GN ENVELOPE GLYCOPROTEIN (FRAGMENT).
 ENV. Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;
 RA NCBI

RC STRAIN=FROM N.A.
 RD SEQUENCE FROM N.A.

RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR INTERPRO: IPR000777;
 DR PFM: PFM0516; GP120.1;

DR PFM: PFM0517; GP41.1;
 KW Envelope protein.
 FT NON_TER 418
 SQ SEQUENCE 418 AA; 47882 MW; 2ADF5E8FE577281 CRC64;

Query Match 92.0%; Score 162; DB 12; Length 418;

Best Local Similarity 81.2%; Pred. No. 2, 5e-16;
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONQOLLINMGCRGRILVCYTSVNNER 32
|||||:|||||:|||||:|||||:|||||
DB 335 ALETLIONQOLLINMGCRGRILVCYTSVNNER 366

RESULT 15

ID 057074 PRELIMINARY: PRT: 871 AA.
057074

AC 057074: 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, last annotation update)

DE ENVELOPE GLYCOPROTEIN.

OS HIV Immunodeficiency virus type 1.

CC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_Taxid=11676.

[11]

SEQUENCE FROM N.A.

RC STRAIN-SAMPLE 655HA;

RA Hunt J.C., Golden A.M., Lund J.K., Gurtler L.G., Zekeng L., Odiang J.,

RA Kapile L., Hampel H., Vallier A., Devere S.G.,

RA Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.

DR D83102.1 (2483483, 316, 1);

DR INTERPRO: IPR000777; -;

DR PFAM: PF00516; GP120; 1.

DR PFAM: PF00517; GP41; 1.

KW Envelope protein.

SO SEQUENCE 871 AA; 97964 MW; F0C9UD8592D23358 CRC64;

Query Match

92.0%; Score 162; DB 12; Length 871;

Best Local Similarity 84.4%; Pred. No. 5, 2e-16;

Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONQOLLINMGCRGRILVCYTSVNNER 32
|||||:|||||:|||||:|||||:|||||

DB 592 ALETLIONQOLLINMGCRGRILVCYTSVNNES 623

Search completed: March 22, 2001, 10:00:46
Job time: 525 sec

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GenCore version 4.5
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OH protein - protein search, using sw model

Run on: March 22, 2001, 09:57:50 ; Search time 29.4 Seconds
(without alignments)
35,150 Million cell updates/sec

Title: US-09-147-362-12

Perfect score: 176
Sequence: 1 ALSTLLQMDLLIMGCRGLVCTSVNNRNT 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32924092 residues

tal number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum March 08
Maximum March 1008
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	104	64.8	854	1	ENV_SIVC2
2	104	61.3	853	1	ENV_HV122
3	109	61.3	853	1	ENV_HV122
4	108	61.4	843	1	ENV_HV121
5	108	61.4	847	1	ENV_HV121
6	108	61.4	847	1	ENV_HV122
7	108	61.4	851	1	ENV_HV128
8	108	61.4	852	1	ENV_HV128
9	108	61.4	852	1	ENV_HV128
10	108	61.4	853	1	ENV_HV128
11	108	61.4	853	1	ENV_HV128
12	108	61.4	853	1	ENV_HV128
13	108	61.4	856	1	ENV_HV128
14	108	61.4	856	1	ENV_HV128
15	108	61.4	856	1	ENV_HV128
16	108	61.4	856	1	ENV_HV128
17	108	61.4	856	1	ENV_HV128
18	108	61.4	856	1	ENV_HV128
19	108	61.4	856	1	ENV_HV128
20	108	61.4	856	1	ENV_HV128
21	108	61.4	856	1	ENV_HV128
22	106	60.2	848	1	ENV_HV128
23	106	60.2	848	1	ENV_HV128
24	106	60.2	848	1	ENV_HV128
25	106	60.2	848	1	ENV_HV128
26	104	59.7	846	1	ENV_HV128
27	104	59.7	846	1	ENV_HV128
28	104	59.7	846	1	ENV_HV128
29	102	58.0	861	1	ENV_HV128
30	102	58.0	861	1	ENV_HV128
31	96	54.5	859	1	ENV_HV128
32	89.5	50.9	859	1	ENV_HV128
33	89.5	50.9	859	1	ENV_HV128

ALIGNMENTS

Result ID	ENV_SIVC2	STANDARD	PRT	854 AA
1	ENV_SIVC2	01-AUG-1990 (Rel. 15, Created)		
2	ENV_SIVC2	01-AUG-1990 (Rel. 15, Last sequence update)		
3	ENV_SIVC2	15-JUL-1999 (Rel. 38, Last annotation update)		
4	ENV_SIVC2	ENVELOPE POLYPEPTIDE GP120 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE ENVELOPE POLYPEPTIDE GP120), TRANSMEMBRANE GLYCOPROTEIN (GP41).		
5	ENV_SIVC2	Chimpanzee immunodeficiency virus (SIV/cpz2) (CIV).		
6	ENV_SIVC2	Viruses: Retroviridae; Retroviridae; Lentivirus.		
7	ENV_SIVC2	SEQUENCE FROM N.A.		
8	ENV_SIVC2	MDL:LINE-90259077; PubMed-2188136;		
9	ENV_SIVC2	Huet T., Cheyner R., Meyers A., Roelants G., Wain-Hobson S.;		
10	ENV_SIVC2	Genetic organization of a chimpanzee lentivirus related to HIV-1.*;		
11	ENV_SIVC2	Nature 443:356-359(1990).		
12	ENV_SIVC2	STABILITY: STRONG, WITH HIV-1 ENV POLYPEPTIDE.		
13	ENV_SIVC2	*****		
14	ENV_SIVC2	This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch .		
15	ENV_SIVC2	EMBL: X52150; CMA36407.1;		
16	ENV_SIVC2	PIR: S09990; VCLAST;		
17	ENV_SIVC2	HIV: X52154; ENVSCP2;		
18	ENV_SIVC2	INTERPRO: IPR000328;		
19	ENV_SIVC2	INTERPRO: IPR000777;		
20	ENV_SIVC2	PFAM: PF00516; GP120.1;		
21	ENV_SIVC2	DBS: Coe protein; Polypeptide; Glycoprotein; Transmembrane; SIGNAL.		
22	ENV_SIVC2	CHAIN	31	500
23	ENV_SIVC2	TRANSMEM	501	854
24	ENV_SIVC2	TRANSMEM	501	517
25	ENV_SIVC2	TRANSMEM	675	633
26	ENV_SIVC2	TRANSMEM	805	821
27	ENV_SIVC2	TRANSMEM	134	134
28	ENV_SIVC2	CARBOHYD	143	143
29	ENV_SIVC2	CARBOHYD	154	154
30	ENV_SIVC2	CARBOHYD	158	158
31	ENV_SIVC2	CARBOHYD	166	166
32	ENV_SIVC2	CARBOHYD	195	195
33	ENV_SIVC2	CARBOHYD	239	239
34	ENV_SIVC2	CARBOHYD	250	250
35	ENV_SIVC2	CARBOHYD	257	257
36	ENV_SIVC2	CARBOHYD	269	269
37	ENV_SIVC2	CARBOHYD	299	299
38	ENV_SIVC2	CARBOHYD	331	331
39	ENV_SIVC2	CARBOHYD	331	331
40	ENV_SIVC2	CARBOHYD	331	331
41	ENV_SIVC2	CARBOHYD	331	331
42	ENV_SIVC2	CARBOHYD	331	331
43	ENV_SIVC2	CARBOHYD	331	331
44	ENV_SIVC2	CARBOHYD	331	331
45	ENV_SIVC2	CARBOHYD	331	331

```

CC FT CARBOHYD 157 153 N-LINKED (GLCNAc ) (POTENTIAL)
CC FT CARBOHYD 157 157 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 185 185 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 188 188 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 198 196 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 202 202 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 242 242 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 263 263 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 277 277 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 290 290 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 296 296 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 331 331 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 338 338 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 353 353 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 384 384 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 400 400 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 441 441 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 445 445 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 458 458 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 459 459 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 462 462 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 608 608 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 613 613 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 622 622 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 631 631 N-LINKED (GLCNAC ) (POTENTIAL)
CC FT CARBOHYD 671 671 N-LINKED (GLCNAC ) (POTENTIAL)
SO SEQUENCE 853 AA; 97043 MW; 849BDBBCAFAFF7008 CRC64;

Query Match      61.9%; Score 109; DB 1; Length 853;
Best Local Similarity 56.2%; Pred. No. 2.3e-08;
Matches 18; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

OY    1 ALPTLNDQNLINIRGCRHLYCTSYRARNET 32
Db     579 AYERIKQQDLICMGCSKGLCTTTPWANS 610

RESULT   3
ID       ENV_HVJ126          STANDARD; FRT: 855 AA.
AC       P03580-1987 (Rel.: 05 Created)
DT       13-AUG-1987 (Rel.: 05 Sequence update)
RX       Schobertman A., Chutchen C., Kalyandaraman V.S., Lucif P.A.,
RA       Sanchez-Pescador R.;
RT       "Molecular characterization of Human Immunodeficiency virus from
RT       zaire: nucleotide sequence analysis identifies conserved and variable
RL       domains in the envelope gene."
RL       Gene 52:71-82(1987).
CC CC
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CC or send an email to licenses@ebi.ac.uk)

CC -----EMBL: K03458; AAA5380.1;-----
CC PIR: D26192; VCLZJR.
CC HIV: K03458; EVNS56.
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INTERPRO: IPR000328; -
 DR PIR: H44001; H44001; -
 DR INTERPRO: IPR000777; -
 DR PIR: P000516; GP120; 1.
 DR PFAM: P000517; GP41; 1.
 KW AIDS: Coat protein; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 510
 FT CHAIN 511 835
 FT DISULFID 118 207
 FT DISULFID 125 158
 FT DISULFID 130 155
 FT DISULFID 220 249
 FT DISULFID 230 241
 FT DISULFID 298 332
 FT DISULFID 378 444
 FT DISULFID 385 417
 FT CARBOHYD 135 156
 FT CARBOHYD 140 140
 FT CARBOHYD 145 145
 FT CARBOHYD 154 154
 FT CARBOHYD 158 158
 FT CARBOHYD 186 189
 FT CARBOHYD 189 189
 FT CARBOHYD 199 199
 FT CARBOHYD 226 226
 FT CARBOHYD 244 244
 FT CARBOHYD 264 264
 FT CARBOHYD 278 278
 FT CARBOHYD 291 291
 FT CARBOHYD 297 297
 FT CARBOHYD 333 333
 FT CARBOHYD 340 340
 FT CARBOHYD 355 355
 FT CARBOHYD 385 385
 FT CARBOHYD 398 398
 FT CARBOHYD 404 404
 FT CARBOHYD 443 443
 FT CARBOHYD 447 447
 FT CARBOHYD 460 460
 FT CARBOHYD 461 461
 FT CARBOHYD 464 464
 FT CARBOHYD 615 615
 FT CARBOHYD 624 624
 FT CARBOHYD 636 636
 FT CARBOHYD 673 673
 SQ SEQUENCE 855 AA: 96971 MM: 384D306239C3457 CRC64;
 Query Match 51.98; Score 109; DB 1; Length 855;
 Best Local Similarity 55.28; Pred. No. 2, 3e-08;
 Matches 18; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 1 ALETLIAQDOLLINIGRCGRCAVCYSVNMET 32
 DB 581 AVERLYKDDQLLIGWCSGKLCITTVNMSS 612
 RESULT 4
 ENV_HYV12 STANDARD: PRT: 843 AA.
 AC P35561;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
 DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).

CC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-33021387; PubMed-1404605;
 RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
 Shaw G.M.;
 FT *Complete nucleotide sequence, genome organization, and biological
 FT properties of human immunodeficiency virus type 1 in vivo: evidence
 FT for a single virus and complementation.
 FT J Virol 66:6587-6600(1992)
 CC -----
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 CC or send an email to license@isb.slb.ch)
 CC -----
 CC EMBL: M93258; -; NOT ANNOTATED_CDS.
 DR PIR: H44001; H44001;
 DR INTERPRO: IPR000328; -
 DR INTERPRO: IPR000777; -
 DR PFAM: P000516; GP120; 1.
 DR PFAM: P000517; GP41; 1.
 KW AIDS: Coat protein; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 489
 FT CHAIN 490 843
 FT TRANSMEM 738 753
 FT DISULFID 53 73
 FT DISULFID 118 201
 FT DISULFID 125 152
 FT DISULFID 130 153
 FT DISULFID 224 235
 FT DISULFID 292 336
 FT DISULFID 373 432
 FT DISULFID 380 405
 FT CARBOHYD 87 129
 FT CARBOHYD 125 132
 FT CARBOHYD 132 138
 FT CARBOHYD 154 154
 FT CARBOHYD 158 158
 FT CARBOHYD 184 184
 FT CARBOHYD 193 193
 FT CARBOHYD 230 230
 FT CARBOHYD 237 237
 FT CARBOHYD 258 258
 FT CARBOHYD 262 265
 FT CARBOHYD 291 291
 FT CARBOHYD 297 297
 FT CARBOHYD 327 327
 FT CARBOHYD 351 351
 FT CARBOHYD 381 381
 FT CARBOHYD 389 389
 FT CARBOHYD 395 395
 FT CARBOHYD 400 400
 FT CARBOHYD 440 440
 FT CARBOHYD 450 450
 FT CARBOHYD 458 458
 FT CARBOHYD 598 598
 FT CARBOHYD 603 603
 FT CARBOHYD 612 612
 FT CARBOHYD 624 624
 FT CARBOHYD 803 803
 SQ SEQUENCE 843 AA: 95648 MM: C69D0971G31871 CRC64;
 Query Match 61.4%; Score 108; DB 1; Length 843;
 Best Local Similarity 60.0%; Pred. No. 3, 2e-08;

[illegible]

FT	CARBOHD	401		N-LINKED (GLICNAC . .) (POTENTIAL)
FT	CARBOHD	438		N-LINKED (GLICNAC . .) (POTENTIAL)
FT	CARBOHD	454		N-LINKED (GLICNAC . .) (POTENTIAL)
FT	CARBOHD	602		N-LINKED (GLICNAC . .) (POTENTIAL)
FT	CARBOHD	607		N-LINKED (GLICNAC . .) (POTENTIAL)
FT	CARBOHD	628		N-LINKED (GLICNAC . .) (POTENTIAL)
SO	SEQUENCE	847 AA:	96135 MW:	DAS0131/PD7/PZAB CRG4;
Query Match		61.4%	Score 108; DB 1;	Length 847;
Best Local Similarity		60.0%	Pred. No. 3; 2e-08;	
Matches 18;		Conservative	6;	Mismatches 6;
				Indels 0;
				Gaps 0
Oy	1 ALETLONOLINIMCRGACTYSPRN 30 1 : 1 ::::: 11111111111111111111			
Db	573 AVERXKLDQDLGIWGSGRLCTTAVPN 602			
RESULT 6				
ID	ENVJMVW2	STANDARD;	PRT:	847 AA.
AC	P05880;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DE	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ENVELOPE POLYPEPTIDE GLI60 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE			
DE	GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).			
OS	Human immunodeficiency virus type 1 (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirinae.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MDLINE-86235450; Pubmed-3012778;			
RA	Rehn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D., P.			
RA	Sabatuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;			
RT	at risk for AIDS". In HIV-TIF/LAV over time in patients with AIDS or			
RL	Science 233:1548-1553(1986).			
CC	-1- MISCELLANEOUS: ISOLATES WM1, WM2, AND WM3 OBTAINED FROM			
CC	BLOOD SAMPLES SPONTANEOUSLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO			
CC	WAS PERMANENTLY INFECTED BY HER MOTHER.			
CC				
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CC	entities requires a license agreement. (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch)			
DR	EMBL: M12507; AAB12990.1; ..			
DR	GENBANK: M12507; AAB12990.1; ..			
DR	INTERPRO: IPR000777; ..			
DR	INTERPRO: IPR000777; ..			
DR	PFAM: PF00516; GP120; 1.			
DR	PFAM: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;			
KW	Signal.			
MM				
FT	CHAIN	1	29	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	30	51	TRANSMEMBRANE GLYCOPROTEIN.
FT	CHAIN	502	847	BY SIMILARITY.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	202	BY SIMILARITY.
FT	DISULFID	125	193	BY SIMILARITY.
FT	DISULFID	130	152	BY SIMILARITY.
FT	DISULFID	215	244	BY SIMILARITY.
FT	DISULFID	223	236	BY SIMILARITY.
FT	DISULFID	223	236	BY SIMILARITY.
FT	DISULFID	372	435	BY SIMILARITY.
FT	DISULFID	379	408	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLICNAC . .) (POTENTIAL)
FT	CARBOHYD	134	134	N-LINKED (GLICNAC . .) (POTENTIAL)

RA Dandekar S.:
 RT "Biological and molecular characterization of human immunodeficiency
 virus (HIV-189) from the brain of a patient with progressive
 dementia.";
 RL Virology 168:79-89(1999).
 CC -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
 CC HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M21098; AAA4221.1.;
 DR PIR: A1667; VCLJIB.
 DR HIV: M21098; ENVSBRVA.
 DR INTERPRO: IP8000328.;
 DR INTERPRO: IP8000777.;
 DR PFM: PF00516; GP120; 1.
 DR PFM: PF00517; GP41; 1.
 KM AIDS: Coat protein; Glycoprotein; Transmembrane;
 RT Signal.
 RL SIGNAL. 31 30
 FT CHAIN 507
 FT CHAIN 852
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 155
 FT DISULFID 218 247
 FT DISULFID 229 240
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 FT DISULFID 483 412
 FT CARBOHYD 49 49
 FT CARBOHYD 88 88
 FT CARBOHYD 135 135
 FT CARBOHYD 138 138
 FT CARBOHYD 156 156
 FT CARBOHYD 197 197
 FT CARBOHYD 234 234
 FT CARBOHYD 241 241
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 395 395
 FT CARBOHYD 397 397
 FT CARBOHYD 331 331
 FT CARBOHYD 354 354
 FT CARBOHYD 360 360
 FT CARBOHYD 384 384
 FT CARBOHYD 390 390
 FT CARBOHYD 396 396
 FT CARBOHYD 400 400
 FT CARBOHYD 442 442
 FT CARBOHYD 442 442
 FT CARBOHYD 607 607
 FT CARBOHYD 621 621
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 FT CARBOHYD 621 621
 FT CARBOHYD 633 633
 FT CARBOHYD 670 670
 FT CARBOHYD 812 812
 FT CARBOHYD 812 812
 SQ SEQUENCE 852 AA; 97203 MW; 2BB865435DC015F CRO64;

Query Match 51.4% Score 108; DB 1; Length 852;
 Best Local Similarity 60.0%; E-Value 3.2e-06;
 Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALFTLQNGQLATNGCNGKALWCTSYRKN 30
 Db 578 AYERYLKQDGLMGSCSKSLCTTAVPN 607
 RESULT 9
 ID ENV_HV153 STANDARD; PRT; 852 AA.
 DC P19549;1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTRAINS: EXTERIOR MEMBRANE
 GN GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
 OS ENV.
 OC Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
 CC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 RP SOURCE FROM N.A.
 RX MEDLINE-60317906; PubMed-2370668;
 RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.:
 RT "Human immunodeficiency virus type 1 cellular host range,
 RT replication, and cytopathicity are linked to the envelope region of
 the viral genome.";
 RL J. Virol. 64:4016-4020(1990).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J9847; AAA43067.1.;
 DR PIR: A1667; VCLJIB.
 DR INTERPRO: IP8000328.;
 DR INTERPRO: IP8000777.;
 DR PFM: PF00516; GP120; 1.
 DR PFM: PF00517; GP41; 1.
 KM AIDS: Coat protein; Glycoprotein; Transmembrane;
 RT Signal.
 RL SIGNAL. 31 29
 FT CHAIN 507
 FT CHAIN 852
 FT DISULFID 54 74
 FT DISULFID 118 206
 FT DISULFID 125 197
 FT DISULFID 130 156
 FT DISULFID 219 248
 FT DISULFID 229 240
 FT DISULFID 297 331
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[illegible]

us-09-147-362-12.rsp

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us-09-147-362-12.rsp
0;
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us-09-147-362-12.rsp

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:53:45 ; Search time 57.2 Seconds

(without alignments)
37,986 Million cell updates/sec

Title: US-09-147-362-12

Perfect score: 176

Sequence: 1 ALETLQNOOLLINMCGRLVCTSVRNHET 32

Scoring table:

BLOSUM62
Gapop: 10.0 , Gapext: 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 88

Maximum Match 1008

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length DB	ID	Description
1	159	90.3	104	2	S52930	gag ENV protein -
2	155	88.1	863	2	A53034	gag ENV protein -
3	151	85.8	877	2	S49197	gag ENV protein -
4	114	64.8	854	1	VCLJST	env polypeptide pr
5	111	63.1	357	2	S21990	env polypeptide pr
6	111	63.1	357	2	S70423	env polypeptide pr
7	111	63.1	357	2	S22002	env polypeptide pr
8	111	63.1	358	2	S70428	env polypeptide pr
9	111	63.1	358	2	B01621	env polypeptide pr
10	111	63.1	358	2	S70417	env polypeptide pr
11	110	62.5	358	2	S70417	env polypeptide pr
12	109	61.9	443	2	C41621	env polypeptide pr
13	109	61.9	853	2	S54384	env polypeptide pr
14	109	61.9	855	1	VCLJZR	env polypeptide pr
15	108	61.4	357	2	S22006	env polypeptide pr
16	108	61.4	357	2	S21994	env polypeptide pr
17	108	61.4	357	2	S22004	env polypeptide pr
18	108	61.4	357	2	S21996	env polypeptide pr
19	108	61.4	357	2	S70412	env polypeptide pr
20	108	61.4	357	2	S70421	env polypeptide pr
21	108	61.4	358	2	S21998	env polypeptide pr
22	108	61.4	358	2	S70425	env polypeptide pr
23	108	61.4	358	2	S70425	env polypeptide pr
24	108	61.4	445	1	A44001	env polypeptide pr
25	108	61.4	852	1	VCLJBR	env polypeptide pr
26	108	61.4	852	1	S21266	env polypeptide pr
27	108	61.4	852	1	S21266	env polypeptide pr
28	108	61.4	852	1	S21266	env polypeptide pr
29	108	61.4	855	1	VCLJAZ	env polypeptide pr

30	108	61.4	855	1	VCLJH3	env polypeptide pr
31	108	61.4	856	1	VCLJVL	env polypeptide pr
32	108	61.4	856	1	VCLJW	env polypeptide pr
33	108	61.4	861	1	VCLJW	env polypeptide pr
34	108	61.4	861	1	VCLJSC	env polypeptide pr
35	106	60.2	856	1	A44963	env polypeptide pr
36	105	59.7	847	1	VCLJND	env polypeptide pr
37	105	59.7	847	1	T09478	env polypeptide pr
38	105	59.7	847	1	T09478	env polypeptide pr
39	104	59.1	859	1	VCLJH4	env polypeptide pr
40	104	59.1	868	1	VCLJH4	env polypeptide pr
41	102	58.0	729	1	VCLJXK	env polypeptide pr
42	102	58.0	861	1	VCLJXB	env polypeptide pr
43	101	57.4	851	2	S33985	env polypeptide pr
44	96	54.5	859	2	T01672	env polypeptide pr
45	95.5	54.3	855	2	A45713	Env transmembrane

ALIGNMENTS

RESULT 1

gag ENV protein - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 06-Jun-1995 #sequence: revision 1 Jul-1995 #text: change 26-Aug-1999

C:Accession: S52930

A:Description: A novel HIV-1 strain illustrates the diversity of the O group.

A:Reference number: S52929

A:Accession: S52930

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-104 <CON>

A:Cross-References: EMBL: X84328; NID: g695526; PID: CAA59066.1; PTD: g695527

C:Superfamily: Type B retrovirus env polypeptide

Query Match 90.3%; Score 159; DB 2; Length 104;

Best Local Similarity 81.2%; Pred. No. 2.3e-15;

Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLQNOOLLINMCGRLVCTSVRNHET 32

DB 35 ALETLQNOOLLINMCGRLVCTSVRNHET 66

RESULT 2

gag polypeptide - human immunodeficiency virus type 1 (strain Ant10)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 03-May-1994 #sequence: revision 03-May-1994 #text: change 07-May-1999

C:Accession: A53034

A:Description: A novel HIV-1 strain illustrates the diversity of the O group.

A:Reference number: S52929

A:Accession: A53034

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-863 <VAN>

A:Cross-References: GB: L02587

C:Superfamily: Type B retrovirus env polypeptide

C:Keywords: polypeptide

Query Match 88.1%; Score 155; DB 2; Length 863;

Best Local Similarity 81.2%; Pred. No. 6.5e-14;

Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLQNOOLLINMCGRLVCTSVRNHET 32

DB 1 ALETLQNOOLLINMCGRLVCTSVRNHET 32

2
Fri Mar 23 07:47:32 2001

us-09-147-362-12.rpt

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Fri Mar 23 07:47:30 2001

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:52:43 : Search time 46.96 Seconds
(without alignments)

12.236 Million cell updates/sec

Title: US-09-147-362-12

Sequence: 1 ALETLNOLLNIMCGRLVCTVSRNNET 32

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Hit number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA*
1: /cgn2_6/pdata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/pdata/2/1aa/6.COMB.pep:*
3: /cgn2_6/pdata/2/1aa/6.COMB.pep:*
4: /cgn2_6/pdata/2/1aa/6.COMB.pep:*
5: /cgn2_6/pdata/2/1aa/6.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	165	93.8	215	2	US-08-912-129A-58
2	165	93.8	245	2	US-08-912-129A-46
3	165	93.8	373	2	US-08-912-129A-56
4	165	93.8	490	2	US-08-912-129A-50
5	165	93.8	618	2	US-08-912-129A-54
6	165	93.8	873	2	US-08-912-129A-61
7	162	92.0	40	3	US-08-894-699-39
8	162	92.0	356	1	US-08-602-713-12
9	162	92.0	356	1	US-08-989-493-12
10	162	92.0	41	3	US-08-894-699-37
11	160	90.9	41	3	US-08-894-699-42
12	158	89.8	41	3	US-09-433-428D-10
13	158	89.8	41	3	US-09-433-428D-10
14	157	89.2	40	3	US-08-894-699-40
15	156	88.6	33	3	US-09-433-428D-4
16	156	88.6	33	3	US-09-433-428D-15
17	156	88.6	42	3	US-08-894-699-56
18	155	88.1	33	3	US-09-433-428D-12
19	155	88.1	33	3	US-09-433-428D-8
20	153	86.7	33	3	US-09-433-428D-21
21	153	86.7	33	3	US-09-433-428D-25
22	152	86.4	33	3	US-09-433-428D-27
23	152	86.4	33	3	US-08-894-699-16
24	152	86.4	40	3	US-08-894-699-56
25	151	85.8	33	3	US-09-433-428D-14
26	151	85.8	33	3	US-09-433-428D-14
27	151	85.8	33	3	US-09-433-428D-14
28	151	85.8	33	3	US-09-433-428D-14

29	151	85.8	33	3	US-09-433-428D-26	Sequence 26, Appl
30	151	85.8	33	3	US-08-894-699-41	Sequence 29, Appl
31	151	85.8	41	3	US-08-894-699-41	Sequence 41, Appl
32	150	85.2	33	3	US-09-433-428D-6	Sequence 6, Appl
33	150	85.2	33	3	US-09-433-428D-6	Sequence 6, Appl
34	150	85.2	33	3	US-09-433-428D-6	Sequence 6, Appl
35	150	85.2	33	3	US-09-433-428D-10	Sequence 10, Appl
36	149	84.7	33	3	US-09-433-428D-11	Sequence 11, Appl
37	149	84.7	33	3	US-09-433-428D-11	Sequence 11, Appl
38	149	84.7	33	3	US-09-433-428D-18	Sequence 18, Appl
39	148	83.0	33	3	US-09-433-428D-28	Sequence 28, Appl
40	148	83.0	33	3	US-09-433-428D-7	Sequence 7, Appl
41	146	83.0	33	3	US-09-433-428D-17	Sequence 17, Appl
42	146	83.0	33	3	US-09-433-428D-20	Sequence 20, Appl
43	146	83.0	33	3	US-09-433-428D-20	Sequence 20, Appl
44	146	83.0	33	3	US-09-433-428D-22	Sequence 22, Appl
45	146	83.0	35	1	US-08-470-202-62	Sequence 62, Appl

ALIGNMENTS

```

RESULT 1
US-08-912-129A-58
: Sequence 58, Application US/08912129A
: Patent No. 5925233
: GENERAL INFORMATION:
: APPLICANT: VALLART, ANADRUZELA S.
: APPLICANT: HACKETT, JOHN JR.
: APPLICANT: HICKMAN, ROBERT K.
: APPLICANT: VARTER, VINCENT A. JR.
: APPLICANT: NECKLAMS, ELIZABETH A.
: APPLICANT: GOLDEN, ALAN HAZELINE A.
: APPLICANT: BERKMAN, SUSIL G.
: APPLICANT OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
: NUMBER OF SEQUENCES: 89
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Abbott Laboratories
: STREET: 100 Abbott Park Road
: CITY: Abbott Park
: STATE: IL
: COUNTRY: USA
: COMPUTER FILE NO: 6064-3500
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
: OPERATING SYSTEM: IBM Compatible
: SOFTWARE: Microsoft Word (ASCII format output)
: CURRENT APPLICATION DATA: 08/912.129A
: PRIORITY DATA: 436
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Dancigers, Andreas M.
: REGISTRATION NUMBER: 212
: REPRESENTATION INFORMATION: 6109 US, 01
: TELEPHONE: 847-937-9803
: TELEFAX: 847-938-2623
: TELEX:
: INFORMATION FOR SEQ ID NO: 58:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 215 amino acids
: TOPOLOGY: single
: US-08-912-129A-58

```

Query Match 93.8%; Score 165; DB 2; Length 215;
Best Local Similarity 84.4%; Pred. No. 2,76-17;

Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLQNDOLNMGCRGLVCTSVKNNET 32
DB 117 ALETLQNDOLNMGCRGLVCTSVKNNET 148

RESULT 2
US-08-912-129A-48
Sequence 48, Application US/08912129A

Patent No. 5922533
GENERAL INFORMATION:

APPLICANT: VALLARI, ANDRUZELA S.

APPLICANT: HACKETT, JOHN JR.

APPLICANT: HICKMAN, ROBERT K.

APPLICANT: VARIER, VINCENT A. JR.

APPLICANT: NESKANS, ELIZABETH A.

APPLICANT: GOLDEN, ALAN M.

APPLICANT: BRENNAN, CATHERINE A.

APPLICANT: DEVARE, SUSHL G.

TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:

ADDRESS: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch diskette, 1.44 MB

OPERATING SYSTEM: MS-DOS (Windows 95)

SOFTWARE: Microsoft Word (ASCII format output)

CURRENT APPLICATION DATA: US/08/912,129A

APPLICATION NUMBER: 32,652

FILING DATE: 15-AUG-1997

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Danckerts, Andreas M.

REGISTRATION NUMBER: 32,652

REFERENCE/DOCKET NUMBER: 6109, US, 01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-938-9803

TELEFAX: 847-938-2623

INFORMATION FOR SEQ. ID NO. 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 245 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-912-129A-48

Patent No. 5922533

GENERAL INFORMATION:

APPLICANT: VALLARI, ANDRUZELA S.

APPLICANT: HACKETT, JOHN JR.

APPLICANT: HICKMAN, ROBERT K.

APPLICANT: VARIER, VINCENT A. JR.

APPLICANT: NESKANS, ELIZABETH A.

APPLICANT: GOLDEN, ALAN M.

APPLICANT: BRENNAN, CATHERINE A.

APPLICANT: DEVARE, SUSHL G.

TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:

ADDRESS: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch diskette, 1.44 MB

OPERATING SYSTEM: MS-DOS (Windows 95)

SOFTWARE: Microsoft Word (ASCII format output)

CURRENT APPLICATION DATA: US/08/912,129A

APPLICATION NUMBER: 32,652

FILING DATE: 15-AUG-1997

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Danckerts, Andreas M.

REGISTRATION NUMBER: 32,652

REFERENCE/DOCKET NUMBER: 6109, US, 01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-938-9803

TELEFAX: 847-938-2623

INFORMATION FOR SEQ. ID NO. 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 373 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-912-129A-52

Query Match 93.8%; Score 165; DB 2; Length 373;
Best Local Similarity 84.4%; Pred. No. 56-17;

Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLQNDOLNMGCRGLVCTSVKNNET 32
DB 117 ALETLQNDOLNMGCRGLVCTSVKNNET 148

RESULT 4
US-08-912-129A-50
Sequence 60, Application US/08912129A

Patent No. 5922533
GENERAL INFORMATION:

APPLICANT: VALLARI, ANDRUZELA S.

APPLICANT: HACKETT, JOHN JR.

APPLICANT: HICKMAN, ROBERT K.

APPLICANT: VARIER, VINCENT A. JR.

APPLICANT: NESKANS, ELIZABETH A.

APPLICANT: GOLDEN, ALAN M.

APPLICANT: BRENNAN, CATHERINE A.

APPLICANT: DEVARE, SUSHL G.

TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS (Windows 95)
 SOFTWARE: MICROSOFT WORD (ASCII format output)
 APPLICATION NUMBER: US/08/912.129A
 FILING DATE: 15-AUG-1997
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: DANCIGERS, ANDREAS M.
 REFERENCE/DOCKET NUMBER: 6109, US .01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-937-9803
 TELEFAX: 847-938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 60:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 490 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-912-129A-60

Query Match 93.8% Score 165; DB 2; Length 460;
 Best Local Similarity 84.4%; Freq. Mismatches 6, 3e-17;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETTLNQQLNIMGCRGRNLCYTSVKNMET 32
 |||||:|||||:|||||:|||||:|||||
 DB 362 ALETTLNQQLNIMGCRGRNLCYTSVKNMET 393

RESULT 5
 US-08-912-129A-50
 Patent No. 5922533
 GENERAL INFORMATION:
 APPLICANT: VALLARI, ANADRUZELA S.
 APPLICANT: HACKETT, JOHN JR.
 APPLICANT: HICKMAN, ROBERT K.
 APPLICANT: VARTER, VINCENT A. JR.
 APPLICANT: NECKLANS, ELIZABETH A.
 APPLICANT: BRENNAN, CATHERINE A.
 APPLICANT: DEVARE, SUSHIL G.
 TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
 NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS (Windows 95)
 SOFTWARE: MICROSOFT WORD (ASCII format output)
 APPLICATION NUMBER: US/08/912.129A
 FILING DATE: 15-AUG-1997
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: DANCIGERS, ANDREAS M.
 REFERENCE/DOCKET NUMBER: 6109, US .01
 TELECOMMUNICATION INFORMATION:

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/912.129A
 FILING DATE: 15-AUG-1997
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: DANCIGERS, ANDREAS M.
 REFERENCE/DOCKET NUMBER: 6109, US .01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-937-9803
 TELEFAX: 847-938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 490 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-912-129A-50

Query Match 93.8% Score 165; DB 2; Length 490;
 Best Local Similarity 84.4%; Freq. Mismatches 6, 2e-17;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETTLNQQLNIMGCRGRNLCYTSVKNMET 32
 |||||:|||||:|||||:|||||:|||||
 DB 362 ALETTLNQQLNIMGCRGRNLCYTSVKNMET 393

RESULT 6
 US-08-912-129A-54
 Patent No. 5922533
 GENERAL INFORMATION:
 APPLICANT: VALLARI, ANADRUZELA S.
 APPLICANT: HACKETT, JOHN JR.
 APPLICANT: HICKMAN, ROBERT K.
 APPLICANT: VARTER, VINCENT A. JR.
 APPLICANT: NECKLANS, ELIZABETH A.
 APPLICANT: BRENNAN, CATHERINE A.
 APPLICANT: DEVARE, SUSHIL G.
 TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
 NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS (Windows 95)
 SOFTWARE: MICROSOFT WORD (ASCII format output)
 APPLICATION NUMBER: US/08/912.129A
 FILING DATE: 15-AUG-1997
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: DANCIGERS, ANDREAS M.
 REFERENCE/DOCKET NUMBER: 6109, US .01
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-937-9803
TELEFX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-54

Query Match 93.8%; Score 165; DB 2; Length 618;
Best Local Similarity 84.4%; Pred. No. 8-7e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLINMCKGRGLCYTSVKNMET 32
362 ALETLIONOOLLINMCKGRGLCYTSVKNMET 393

RESULT 7

US-08-912-129A-61
Sequence 61, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K. JR.
APPLICANT: KANTER, VINCENT A.
APPLICANT: NIKAM, VIRENDRA A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
OPERATING SYSTEM: IBM compatible
SOFTWARE: MICROSOFT WORD (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912.129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
PRIORITY NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109 US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 873 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-61

Query Match 93.8%; Score 165; DB 2; Length 873;
Best Local Similarity 84.4%; Pred. No. 1.3e-16;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLINMCKGRGLCYTSVKNMET 32
591 ALETLIONOOLLINMCKGRGLCYTSVKNMET 622

RESULT 8

US-08-894-699-39
Sequence 39, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSI, SENROB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LI, THOAI-DUNG
APPLICANT: CHEN, ANDREW
TITLE OF INVENTION: GROUP OF HIV-1 FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD, Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894.699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 28-FEB-1996
PRIOR APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-2200
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-39

Query Match 92.0%; Score 162; DB 3; Length 40;
Best Local Similarity 87.5%; Pred. No. 1.1e-17;
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLINMCKGRGLCYTSVKNMET 32
9 ALETLIONOOLLINMCKGRGLCYTSVKNMET 40


```

RESULT 9
US-08-602-713-12
: Sequence 12, Application US/08602713
: Patent No. 5798205
: GENERAL INFORMATION:
: APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan;
: APPLICANT: G Riller, Latz G.; Eberle, Josef; Kaplue, Lazare;
: APPLICANT: Zekeng, L opold Achengui
: TITLE OF INVENTION: Retrovirus from The HIV Group And Its Use
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Felfe & Lynch
: STREET: 805 Third Avenue
: CITY: New York City
: STATE: New York
: COUNTRY: USA
: PRIORITY INFORMATION:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: PC-DOS
: SOFTWARE: Wordperfect
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/602,713
: FILING DATE: 16-FEBRUARY-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 195 05 262
: FILING DATE: 16-FEBRUARY-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Hanson, No. 5798205man D.
: REGISTRATION NUMBER: 30,946
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 688-9200
: TELEFAX: (212) 688-9384
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 356 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: Protein
: FRAGMENT TYPE: Internal
US-08-602-713-12

Query Match          92.0%; Score 162; DB 1; Length 356;
Best Local Similarity 81.2%; Pred. No. 1.3e-16;
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNQQOLLNMGCRGLCYTSVMNET 32
DB 312 ALETLNQQOLLNMGCRGLCYTSVMNET 343

RESULT 10
US-08-989-493-12
: Sequence 12, Application US/08989493
: Patent No. 6162831
: GENERAL INFORMATION:
: APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan;
: APPLICANT: G Riller, Latz G.; Eberle, Josef; Kaplue, Lazare;
: APPLICANT: Zekeng, L opold Achengui
: TITLE OF INVENTION: Retrovirus from The HIV Group And Its Use
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Felfe & Lynch
: STREET: 805 Third Avenue
: CITY: New York City
: STATE: New York

```

```

: COUNTRY: USA
: ZIP: 10022
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: PC-DOS
: SOFTWARE: Wordperfect
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/989,493
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/602,713
: FILING DATE: 16-FEBRUARY-1996
: APPLICATION NUMBER: DE 195 05 262
: FILING DATE: 16-FEBRUARY-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Hanson, No. 6162831man D.
: REGISTRATION NUMBER: 30,946
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 688-9200
: TELEFAX: (212) 688-9384
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 356 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: Protein
: FRAGMENT TYPE: Internal
US-08-989-493-12

Query Match          92.0%; Score 162; DB 3; Length 356;
Best Local Similarity 81.2%; Pred. No. 1.3e-16;
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNQQOLLNMGCRGLCYTSVMNET 32
DB 312 ALETLNQQOLLNMGCRGLCYTSVMNET 343

RESULT 11
US-08-894-699-67
: Sequence 67, Application US/08894699
: Patent No. 6160956
: GENERAL INFORMATION:
: APPLICANT: SIMON, FRANCOIS
: APPLICANT: SARACOSTI, SEMTOS
: APPLICANT: LOUSSEY-ALJAK, IBRITSSAM
: APPLICANT: LY, THOAI-DUONG
: APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
: TITLE OF INVENTION: GROUP O HIV-1 FRAGMENTS OF SUCH
: NUMBER OF SEQUENCES: 61
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
: STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
: STREET: FLOOR
: CITY: ARLINGTON
: STATE: VA
: COUNTRY: USA
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/894,699
: FILING DATE: 01-DEC-1997

```

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR96/00294
 FILING DATE: 26-FEB-1996
 PRIOR APPLICATION DATA: FR 95/02236
 FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,614
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 1
 SEQUENCE CHARACTERISTICS:
 LENGTH: 41 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-994-699-67

Query Match 80.9% Score 160; DB 3; Length 41;
 Best Local Similarity 81.2% Pred. No. 2,3e-17;
 Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALETLIQNQLLMGKGRGLCTYSVKWNET 32
 DB 9 ALETLIQNQLLMGKGRGLCTYSVKWNET 40

RESULT 12
 US-08-994-699-37
 Sequence 37, Application US/08994699
 Patent No. 6030769
 GENERAL INFORMATION:
 APPLICANT: SIMON, FRANCOIS
 APPLICANT: SARAGOSTI, SEBAST
 APPLICANT: LOUSSERT-AJAKA, IBITISSAM
 APPLICANT: LY, THOI-DUONG, MARIE-LAURE
 APPLICANT: CHAIX-BADIER, MARIE-LAURE
 TITLE OF INVENTION: FRAGMENTS OF SUCH
 TITLE OF INVENTION: VIRUSSES, AND USES THEREOF
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESS: P.C.
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 STREET, FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/994,699
 FILING DATE: 01-DEC-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR96/00294
 FILING DATE: 26-FEB-1996
 PRIOR APPLICATION DATA: FR 95/02236
 FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,614
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 1
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-994-699-37

Query Match 89.8% Score 158; DB 3; Length 40;
 Best Local Similarity 81.2% Pred. No. 4,4e-17;
 Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALETLIQNQLLMGKGRGLCTYSVKWNET 32
 DB 9 ALETLIQNQLLMGKGRGLCTYSVKWNET 40

RESULT 13
 US-08-994-699-42
 Sequence 42, Application US/08994699
 Patent No. 6030769
 GENERAL INFORMATION:
 APPLICANT: SIMON, FRANCOIS
 APPLICANT: SARAGOSTI, SEBAST
 APPLICANT: LOUSSERT-AJAKA, IBITISSAM
 APPLICANT: LY, THOI-DUONG, MARIE-LAURE
 APPLICANT: CHAIX-BADIER, MARIE-LAURE
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
 TITLE OF INVENTION: VIRUSSES, AND USES THEREOF
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESS: P.C.
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 STREET, FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/994,699
 FILING DATE: 01-DEC-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR96/00294
 FILING DATE: 26-FEB-1996
 PRIOR APPLICATION DATA: FR 95/02236
 FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,614
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

CC M80459-74 represent synthetic peptides (either linear or cyclized by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 XX
 SO Sequence 32 AA:

Query Match

100.0%; Score 176; DB 19; Length 32;

Best Local Similarity 100.0%; Pred. No. 4, 9e-17;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNQGLINMGCRGLVCYSYRNMT 32

DB 1 aletlmgqlinmgcrgrlvcysyrnmt 32

RESULT 2

M80469 standard; peptide: 32 AA.

M80469;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

M0945323-A1.

15-OCT-1998.

06-APR-1998; 98MO-FR00691.

24-FEB-1998; 98FR-0002212.

09-APR-1997; 97FR-0004356.

(SNF1) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by

human immune deficiency virus of group O

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

RESULT 3
 M80471 standard; peptide: 32 AA.
 M80471;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

M0945323-A1.

15-OCT-1998.

06-APR-1998; 98MO-FR00691.

24-FEB-1998; 98FR-0002212.

09-APR-1997; 97FR-0004356.

(SNF1) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by

human immune deficiency virus of group O

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

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human immune deficiency virus (HIV).

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human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

human immune deficiency virus (HIV).

FH Key Location/Qualifiers
 FT Protein 2..46 /note="gp120 sequence"
 FT Peptide 47..245 /note="gp41 sequence"
 FT
 XX MO9909410-A2.
 XX
 XX 25-FEB-1999.
 XX
 XX 07-AUG-1998: 98MO-US16506.
 XX
 XX 15-AUG-1997: 97US-0912129.
 XX
 XX (ABBO) ABBOTT LAB.
 XX
 XX Brennan CA, Devere SC, Golden AM, Hockett JR, Hickman RK:
 XX Necklawa BC, Vallari AS, Veltman V;
 XX
 XX WPI: 1999-190224/16.
 XX N-PSDB: K37193.

PT New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -
 PT can be used in field assay, requiring no electricity and less
 PT specialised equipment

Claim 1: Fig 5: 104pp: English.

The invention relates to a rapid assay for simultaneous detection and
 CC of antibodies to HIV-1 groups O and M, and HIV-2. The
 CC method comprises the steps of: (a) providing a sample containing at
 CC least one immobilised capture reagent, a second analyte and on which the sample
 CC moves from the proximal to the distal end by capillary action, under
 CC conditions sufficient to form capture reagent/analyte complex, under
 CC (b) determining the presence of analyte(s) by detecting a visible colour
 CC change at the capture reagent site on the strip wherein the capture
 CC reagent is a group O comprises a polypeptide shown in Y06977-90 and
 CC Y06983-84; and the group M comprises a polypeptide shown in
 CC Y06982; and that for HIV-2, the group O comprises a polypeptide shown in
 CC Y06981. The invention is used to screen patients for HIV-1 types O and
 CC M, and HIV-2. The invention will be particularly useful for the
 CC situation where equipment and/or electricity is not available. The
 CC invention provides a screening method which is faster and requires less
 CC equipment than prior art methods. The present sequence represents a
 CC capture reagent for HIV-1 group O.
 XX
 XX Sequence 215 AA:

Query Match 93.8%; Score 165; DB 20; Length 215;
 Best Local Similarity 84.4%; Pred. No. 1e-14;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 1 ALEPTLONQOLINMGRCGLGCTYSYRNRET 32
 Db 117 atetllqngllnlwgcgkrllyctskwmet 148

RESULT 7
 Y77374
 ID Y77374 standard: Protein: 215 AA.
 XX
 XX Y77374:
 XX
 XX 22-MAY-2000 (first entry)
 XX
 XX HIV-1 group O env gp120/gp41 pCO-8PL recombinant protein, SEQ ID NO:58.
 XX
 XX HIV-1 group O: env: gp120, gp41, glycoprotein; monoclonal antibody;
 XX Immunassay: positive control; antigen; synthetic gene construction; mutagen;
 XX Escherichia coli: antigen; synthetic gene construction; mutagen;
 KW deletion mutation.

XX
 OS Human immunodeficiency virus type 1 group O isolate HAM112.
 OS Synthetic.
 XX
 XX MO200004383-A2.
 XX
 XX 27-JAN-2000.
 XX
 XX 09-JUL-1999: 99MO-US15469.
 XX
 XX 14-JUL-1998: 98US-0115171.
 XX
 XX (ABBO) ABBOTT LAB.
 XX
 XX Schefel JM, Hockett JR, Tyner JD, Hickman RK:
 XX WPI: 2000-171290/15.
 XX N-PSDB: 290285.
 XX
 XX Novel monoclonal antibodies useful as positive control reagent for
 XX detecting human immunodeficiency virus infections and diagnosing,
 XX evaluating or prognosing viral disease -
 XX Example 3: Fig 5: 148pp: English.

The invention relates to anti-HIV-1 group O monoclonal antibodies, which
 CC may be used as positive control reagents in immunoassays to detect and
 CC differentiate HIV-1 infections. The invention also encompasses a
 CC monoclonal antibody which binds specifically to an HIV-1 group O antigen,
 CC which is a protein that crosses reactively to a corresponding antigen
 CC selected from HIV-1 group O antigens and HIV-2 antigens; and a method of
 CC using a monoclonal antibody antigen and HIV-2 antigens; and a method of
 CC immunoassay for the detection of anti HIV-1 control reagent in an
 CC immunoassay for the detection of anti HIV-1 control reagents in the
 CC immunoassays capable of detecting anti-HIV-1 group O antibodies. Such
 CC immunoassays involve coupling a monoclonal antibody with HIV group-1
 CC antibodies of the invention should be used to ensure that the reagents
 CC provided to detect HIV-1 group O antigens are specific. The monoclonal
 CC monoclonal antibodies may also can be immunoprecipitating property. The
 CC cell cultures or biological tissues. The monoclonal antibodies can also
 CC be used for generating chimeric antibodies for therapeutic use. Different
 CC antibodies of HIV antigens can be used in combination in assay to diagnose,
 CC evaluate, or prognose HIV-1 infection. The monoclonal
 CC antibodies are also useful for detecting HIV-1 group O antigens
 CC from HIV-group M and HIV-2 antigens sequencing H77369-70 and H77374-75
 CC recombinant HIV-1 group O env antigens encoded by the synthetic genes
 CC 290280-290286. The recombinant HIV-1 env proteins contain various
 CC deletions relative to the native HAM112 isolate env protein (Y77376). The
 CC recombinant HIV-1 group O antigens were purified and used to screen
 CC hybridoma cultures.
 XX
 XX Sequence 215 AA:

Query Match 93.8%; Score 165; DB 21; Length 215;
 Best Local Similarity 84.4%; Pred. No. 1e-14;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 1 ALEPTLONQOLINMGRCGLGCTYSYRNRET 32
 Db 117 atetllqngllnlwgcgkrllyctskwmet 148

RESULT 8
 Y09493
 ID Y09493 standard: Protein: 245 AA.
 XX
 XX Y09493:
 XX
 XX 15-JUL-1999 (first entry)

DE HIV-1 Group O env polypeptide pCO-9pL.

XX HIV; human immunodeficiency virus antigen detection; antibody;
XX differentiation; Group O; env; immunogen; immunoassay.

XX human immunodeficiency virus type 1.

XX WO909179-A2.

XX 25-FEB-1999.

XX 17-AUG-1998: 98MO-US17014.

XX 15-AUG-1997: 97US-0911824.

XX (ABBO) ABBOTT LAB.

XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;

XX WPI: 1999-190167/16.

XX N-PSDB: X56074.

XX New isolated HIV-1 Group O env polypeptides - used for the
XX detection of anti-HIV antibodies and for the production of
XX antibodies for use in detection, purification and therapy

XX Claim 16; Fig 7; 138pp; English.

XX The present invention describes (A) an isolated HIV-1 Group O env
XX polypeptide. Also described is an isolated HIV-1 Group O env
XX polypeptide comprising an immunoreactive portion of a polypeptide as in
XX (1) or (2); an antigen construct comprising a first HIV-1 Group O env polypeptide
XX fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct
XX comprising a fusion of at least one HIV-1 Group O env polypeptide with at
XX least one HIV-1 Group M env polypeptide; (5) an antigen construct
XX comprising a fusion of a first HIV-1 env polypeptide, second (6) an
XX antigen construct comprising a fusion of a first HIV-1 env polypeptide fused to a
XX second HIV-1 env polypeptide; (7) a PN encoding an antigen construct as
XX in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a
XX host cell transformed by an expression vector as in (8); and (10) an
XX immunosay kit for the detection of antibodies to HIV-1 comprising an
XX antigen construct as in (3)-(6). The antigen constructs can be used for
XX the detection of anti-HIV-1 antibodies in test samples. They can also be
XX used as immunogens to produce antibodies. The antigen constructs can be used to
XX purify HIV polypeptides, for therapy and for detection of HIV
XX polypeptides.

XX Sequence 245 AA:

XX Query Match 93.8%; Score 165; DB 20; Length 245;

XX Best Local Similarity 84.4%; Pred. No. 1,2e-14;

XX Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

XX 1 ALETLNNOGLNTMGRCRLVCTYSVRRNMT 32

XX 117 ALETLNNOGLNTMGRCRLVCTYSVRRNMT 148

XX Db 117 ALETLNNOGLNTMGRCRLVCTYSVRRNMT 148

XX RESULT 9

XX Y06977 standard; Protein: 245 AA.

XX Y06977;

XX 06-JUL-1999 (first entry)

XX Recombinant pCO-9pL protein.

XX HIV-1; HIV-2; Immobilised capture reagent; capillary action; screening;

XX antibody; assay.

XX Synthetic.

XX Human immunodeficiency virus type 1.

XX Key Location/Qualifiers

XX Protein 2..46

XX Peptide /note="gp120 sequence"

XX /note="gp41 sequence"

XX WO909410-A2.

XX 25-FEB-1999.

XX 07-AUG-1998: 98MO-US16506.

XX 15-AUG-1997: 97US-0912129.

XX (ABBO) ABBOTT LAB.

XX Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;

XX Necklans EC, Vallari AS, Varilek V;

XX WPI: 1999-190224/16.

XX N-PSDB: X37189.

XX New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -

XX specialised equipment

XX Claim 1; Fig 7; 104pp; English.

XX The invention relates to a rapid assay for simultaneous detection and
XX differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The
XX method comprises capturing the sample with a strip containing at
XX least one immobilised capture reagent per analyte and on which the sample
XX moves from the proximal to the distal end by capillary action, under
XX conditions sufficient to form capture reagent/analyte complexes, and
XX (b) determining the presence of analyte(s) by detecting a visible colour
XX change at the capture reagent site on the strip wherein the Y06977-80 and
XX Y06983-84; and that for HIV-2 comprises a polypeptide polypeptide shown in
XX Y06983-84; and that for HIV-2 comprises the polypeptide shown in Y06981. The
XX method is used to screen patients for antibodies to HIV-1 types O and
XX M, and HIV-2. The invention will be particularly useful in places and
XX situation where equipment and/or electricity is not available. The
XX equipment provides a screening method which is faster and requires less
XX equipment than prior art methods. The present sequence represents a
XX amino acid sequence of the recombinant pCO-9pL recombinant protein which
XX acts as a capture reagent for HIV-1 group O.

XX Sequence 245 AA:

XX Query Match 93.8%; Score 165; DB 20; Length 245;

XX Best Local Similarity 84.4%; Pred. No. 1,2e-14;

XX Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

XX 1 ALETLNNOGLNTMGRCRLVCTYSVRRNMT 32

XX 117 ALETLNNOGLNTMGRCRLVCTYSVRRNMT 148

XX Db 117 ALETLNNOGLNTMGRCRLVCTYSVRRNMT 148

XX RESULT 10

XX Y77369 standard; Protein: 245 AA.

XX Y77369;

XX 22-MAY-2000 (first entry)

XX HIV-1 group O pCO-9pL-encoded truncated env gp41 protein, SEQ ID NO:48.

XX HIV-1 group O; env: gp120: gp41: glycoprotein: monoclonal antibody:
 RM Immunossay; positive control; affinity purification; therapeutic;
 KM Escherichia coli; antigen: synthetic gene construction; mutin;
 KK detection mutation.
 OS Human immunodeficiency virus type 1 group O isolate HAM112.
 OS Synthetic.
 PN MO200004383-A2.
 PN 27-JAN-2000.
 PD 09-JUL-1999; 99MO-US15465.
 PR 14-JUL-1999; 98MS-0115171.
 PA (ABBO) ABBOTT LAB.
 PF Scheffel JW, Hackett JR, Tyner JD, Hickman RK;
 PK WPI: 2000-171290/15.
 DM NP-SDS: 290280.
 DX Novel monoclonal antibodies useful as positive control reagent for
 PT detecting human immunodeficiency virus infections and diagnosing,
 PT evaluating or prognosing viral disease.
 XX
 XX
 XX Example 3: Page 120-121; 148pp: English.
 XX
 XX The invention relates to anti-HIV-1 group O monoclonal antibodies, which
 XX can be used as positive control reagents in immunoassays to detect and
 XX differentiate HIV-1 group O antigens. The invention also encompasses a
 XX monoclonal antibody which binds specifically to an HIV-1 group O antigen,
 XX which has no more than 15% cross reactivity to any other HIV-1 group O
 XX antigen, selected from HIV-1 group M antigens and HIV-2 antigens. The
 XX using a monoclonal antibody as a positive control reagent in an
 XX immunoassay for the detection of anti-HIV-1 group O antibodies. The
 XX monoclonal antibodies are useful as positive control reagents in
 XX immunoassays capable of detecting anti-HIV-1 group O antibodies. Such
 XX antibodies are useful for detecting HIV-1 group O antigens. Such
 XX antigen and detecting the antigen-antibody complex. The monoclonal
 XX antibodies of the invention would be used to detect HIV-1 group O
 XX provided to detect HIV-1 group O antibody were performed. The reagents
 XX monoclonal antibodies may also can be immobilised on a matrix. The
 XX for affinity purification of specific HIV-1 group O-derived proteins from
 XX cell cultures or biological tissues. The monoclonal antibodies can also
 XX be used for generating chimeric antibodies for therapeutic use. Different
 XX epitopes of HIV-1 group O antigens can be used to identify different
 XX evaluate, or prognosticate HIV-1 group O antigens. The monoclonal
 XX antibodies are also useful for differentiating HIV-1 group O antigens
 XX from HIV-1 group M and HIV-2 antigens. Sequences Y77369, Y77370, Y77371,
 XX recombinant HIV-1 group O env antigens encoded by the synthetic genes
 XX Z90280-290286. The recombinant HIV-1 env proteins contain various
 XX deletions relative to the native HAM112 isolate env protein (Y77376). The
 XX recombinant HIV-1 group O antigens were purified and used to screen
 XX hybridoma cultures.
 XX
 XX Sequence 245 AA:
 SO
 01 Query Match 93.8%; Score 165; DB 21: Length 245:
 02 Best Local Similarity 84.4%; Pred. No. 1,26-14;
 03 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 04 1 ALETLAOLGOLALITMCRGRHLYCTVSYRNKCT 32
 05 ALETLAOLGOLALITMCRGRHLYCTVSYRNKCT 32
 06 117 ALETLAOLGOLALITMCRGRHLYCTVSYRNKCT 148
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[illegible]

```

DT      15-JUL-1999   (first entry)
DE      HIV-1 Group O env polypeptide pCO-11PL.
KM      HIV; human immunodeficiency virus; antigen; detection; antibody;
XX      differentiation; Group O; env; Immunogen; Immunoassay.
OS      Human immunodeficiency virus type 1.
PN      MO9090179-AZ.
PD      25-FEB-1999.
PC      17-AUG-1998;    98MO-USI7014.
PE      15-AUG-1997;    97US-0911824.
PX      (ABRO ) ABBOTT LAB.
PY      Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J.;
DR      WPI: 1999-190167/16.
DX      N-PDB#; K56076.
XX      New isolated HIV-1 Group O env polypeptides - used for the
PF      detection of anti-HIV antibodies and for the production of
PT      antipeptides for use in detection, purification and therapy
PS      Claim 15; Fig 9; 138pp; English.
CC      The present invention describes (*) an isolated HIV-1 Group O env
CX      polypeptide. Also described are: (1) an isolated HIV-1 Group O env
CC      polypeptide comprising an immoreactive portion of a polypeptide as in
CC      (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);
CC      (3) an antigen construct comprising a first HIV-1 Group O env polypeptide
CC      fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct
CC      consisting of a fusion of a first HIV-1 group O env polypeptide with at
CC      least one HIV-1 Group M env polypeptide; (5) an antigen construct with at
CC      comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env
CC      polypeptide, and at least one additional HIV-1 polypeptide; (6) an
CC      antigen construct comprising a first HIV-2 env polypeptide fused to a
CC      second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as
CC      in (3)-(6); (8) an expression vector comprising a PV as in (7); (9) a
CC      host cell transformed by an expression vector as in (8); and (10) an
CC      immunoassay kit for the detection of antibodies to HIV-1 comprising an
CC      antigen construct as defined herein. These constructs can be used for
CC      the detection of anti-HIV-1 antibodies in "test samples". They can also be
CC      used as immunogens to produce antibodies. The antibodies can be used to
CC      purify HIV polypeptides, for therapy and for detection of HIV
CC      polypeptides.
SX      Sequence     373 AA:
SQ      Query Match          93.8%: Score 165; DB 20; Length 373;
        Local Similarity  93.4%; Pident No 1; E=1e-140
Matches 277; Conservative         8; Mismatches 50; Indels 0; Gaps 0
OR      1 ALPETHLQGLINIMWCGIRGVYVYS/RNNET 32
       Db | 117 alatlgnqqlnlmgwcygxlrytsyknel 148
RESULT 13
XN      106979
XX      106979 standard; Protein: 373 AA.
MC      Y06979;
DD      06-JUL-1999   (first entry)
RE      Recombinant pCO-11PL protein.
DE
```

KW	HIV-1; HIV-2; Immobilised capture reagent; capillary action; screening;
KM	antibody; assay.
XX	Synthetic.
OS	Human Immunodeficiency virus type 1.
PA	Key
PD	Location/Qualifiers
PT	Protein
FT	2..46
FT	/note="gp120 sequence"
FT	47..245
FT	/note="gp41 sequence"
XX	
-PN	MD909410-A2.
PD	
XX	25-FEB-1999.
PR	07-AUG-1998:
XX	98MO-U516506.
PR	15-AUG-1997:
XX	97US-0912129.
PA	(ABBO) ABBOTT LAB.
XX	
BX	Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK,
P1	Necklaws EC, Vallier AS, Varitek V;
DR	WP1: 1999-190224/16.
DR	N-PDB: X37191.
PT	New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -
PT	can be used in field assay, requiring no electricity and less
PT	specialised equipment
PS	Claim 1: Fig 9; 104pp: English.
XX	
CC	The invention relates to a rapid assay for simultaneous detection and
CC	differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The
CC	assay comprises the steps of: (a) capturing the sample analyte, or at
CC	least one immobilised capture reagent, either under magnetically or
CC	moves from the proximal to the distal end by capillary action, under
CC	conditions sufficient to form capture reagent/analyte complexes, and
CC	(b) determining the presence of analyte(s) by detecting a visible colour
CC	change at the capture reagent site on the strip wherein the capture
CC	reagent for HIV-1 group O comprises a polypeptide shown in Y06577-80 and
CC	Y06581-84; and that for HIV-1 group M comprises a polypeptide shown in the
CC	Y06582; and that for HIV-2 comprises the polypeptide shown in the
CC	Y06583. The invention will be particularly useful in places and
CC	M, and HIV-2. The invention will be particularly useful in places and
CC	situation where equipment and/or electricity is not available. The
CC	invention provides a screening method which is faster and requires less
CC	equipment than prior art methods. The present sequence represents a
CC	c amino acid sequence of the recombinant pCO-19PL recombinant protein which
CC	acts as a capture reagent for HIV-1 group O.
XX	
XX	Sequence 373 AA:
SQ	
XX	
XX	51.8%: Score 165; DB 20;
XX	Query Match Best Local Similarity 84.4%; Prid. No. 1,8e-14;
XX	Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0
OY	1 ALETLNQNQLINMCRCGRGLCYVSRYNNET 32
Db	117 aletlmgqqlnhlwgcgrgltcysvskwnet 148
RESULT 14	
ID	Y09500 standard; Protein; 460 AA.
AC	Y09500;
JT	15-JUL-1999 (first entry)

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 10:00:46 : Search time 171.82 seconds
(without alignments)
21.829 Million cell updates/sec

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Sequence: 1 ALETLIONOOLLDMGCRNCRVCYTSVNNET 32

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

374700 seqs, 117207915 residues

Searched: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: 1: SP:EMBRL15**
2: SP:Proteobacteria**
3: SP:Fungi**
4: SP:Human**
5: SP:Invertebrate**
6: SP:Mammal**
7: SP:Ornithelle**
8: SP:Plant**
9: SP:Phage**
10: SP:Plant**
11: SP:Plant**
12: SP:Plant**
13: SP:Plant**
14: SP:Unclassified**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	92.0	124	12	091hu7 human immun
2	162	92.0	124	12	091hu1 human immun
3	162	92.0	124	12	091hu3 human immun
4	162	92.0	124	12	091hu2 human immun
5	162	91.5	209	12	091EC2 human immun
6	161	91.5	240	12	091EC3 human immun
7	160	90.9	125	12	091EC4 human immun
8	160	90.9	125	12	091EC5 human immun
9	160	90.9	125	12	091EC6 human immun
10	160	90.9	125	12	091EC7 human immun
11	159	90.3	137	12	091EC8 human immun
12	159	90.3	137	12	091EC9 human immun
13	159	90.3	208	12	091EC10 human immun
14	159	90.3	208	12	091EC11 human immun
15	159	90.3	208	12	091EC12 human immun
16	159	90.3	208	12	091EC13 human immun
17	159	90.3	208	12	091EC14 human immun
18	159	90.3	208	12	091EC15 human immun
19	159	90.3	208	12	091EC16 human immun
20	159	90.3	208	12	091EC17 human immun
21	159	90.3	208	12	091EC18 human immun
22	159	90.3	208	12	091EC19 human immun
23	159	90.3	208	12	091EC20 human immun
24	159	90.3	208	12	091EC21 human immun
25	159	90.3	208	12	091EC22 human immun
26	159	90.3	208	12	091EC23 human immun
27	159	90.3	208	12	091EC24 human immun
28	159	90.3	208	12	091EC25 human immun
29	159	90.3	208	12	091EC26 human immun
30	159	90.3	208	12	091EC27 human immun
31	159	90.3	208	12	091EC28 human immun
32	159	90.3	208	12	091EC29 human immun
33	159	90.3	208	12	091EC30 human immun
34	159	90.3	208	12	091EC31 human immun
35	159	90.3	208	12	091EC32 human immun
36	159	90.3	208	12	091EC33 human immun
37	159	90.3	208	12	091EC34 human immun
38	159	90.3	208	12	091EC35 human immun
39	159	90.3	208	12	091EC36 human immun
40	159	90.3	208	12	091EC37 human immun
41	159	90.3	208	12	091EC38 human immun
42	159	90.3	208	12	091EC39 human immun
43	159	90.3	208	12	091EC40 human immun
44	159	90.3	208	12	091EC41 human immun
45	159	90.3	208	12	091EC42 human immun

ALIGNMENTS

RESULT 1
091hu7 PRELIMINARY: PRT: 124 AA.

AC 091hu7: 01-OCT-2000 (TREMUR1.15, Created)

DT 01-OCT-2000 (TREMUR1.15, Last sequence update)

DT 01-OCT-2000 (TREMUR1.15, Last annotation update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

OR Human immunodeficiency virus type 1.

OC Viruses; Retroviridae; Retroviridae; Lentivirus.

NCBI TaxID:11676.

RN [1]

RP SOURCE FROM N.A.

RC S. Yung C., Gao F., Fonjongo P.N., Zekeng L., van der Groen G.,

RA P. Le Gall, C. Schable C., Lal R.B. and transmembrane regions of HIV

RT "Phylogenetic analysis of protease and transmembrane regions of HIV

type 1 group O." J. Virol. 74:1075-1081(2000).

RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).

DR ENBL, AF229271, AF271914.1.

FT NON-TER 124

FT NON-TER 124

SQ SEQUENCE 124 AA: 15187 MW: 105515F114450F8 CRC64:

Query Match 92.0% Score 162: DB 12: Length 124:
Best Local 27, Conservative 84.4% Pred. NO. 6, 9e-17: Mismatches 0: Indels 0: Gaps 0:

Matches 27, Conservative 84.4% Pred. NO. 6, 9e-17: Mismatches 0: Indels 0: Gaps 0:

DB 23 ALETLIONOOLLDMGCRNCRVCYTSVNNET 32

ID 091hu1 PRELIMINARY: PRT: 126 AA.

AC 091hu1: 01-OCT-2000 (TREMUR1.15, Created)

DT 01-OCT-2000 (TREMUR1.15, Last sequence update)

DT 01-OCT-2000 (TREMUR1.15, Last annotation update)

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DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97ES203;
RA Yang C., Gao F., Fonjuno P.N., Zekeng L., Van der Groen G.,
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RL type 1 group O isolates."
DR EMBL; AF229233; MAF1910.1; .
FT NON_TER 1 126
SO SEQUENCE 126 AA; 15169 MW; 13PB10ECDC0DDD CRC64;

Query Match
Best Local Similarity 92.0%; Score 163; DB 12; Length 126;
Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONQDLDMCKGRCGLVCTSVNMNT 32
DB 30 ALETLIONQDLDMCKGRCGLVCTSVNMNTS 61

RESULT 3.
ID 091E33 PRELIMINARY: PRT: 172 AA.
AC 091E33;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DE 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
GN ENV POLYPEPTIDE, GP41 (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF99;
RA Robertson D., Robertson D., Sandrine S., Christel D., Francois S.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
FT NON_TER 1 172
SO SEQUENCE 172 AA; 20388 MW; 97ZC7AF2A754EB13 CRC64;

Query Match
Best Local Similarity 92.0%; Score 163; DB 12; Length 172;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONQDLDMCKGRCGLVCTSVNMNT 32
DB 26 ALETLIONQDLDMCKGRCGLVCTSVNMNT 57

RESULT 4.
ID 091E32 PRELIMINARY: PRT: 234 AA.
AC 091E32;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DE 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
GN ENV POLYPEPTIDE, GP41 (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.

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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF100;
RA Robertson P., Robertson D., Sandrine S., Christel D., Francois S.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
FT NON_TER 1 234
SO SEQUENCE 234 AA; 27036 MW; 39B050B3F8555N6C CRC64;

Query Match
Best Local Similarity 92.0%; Score 163; DB 12; Length 234;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONQDLDMCKGRCGLVCTSVNMNT 32
DB 46 ALETLIONQDLDMCKGRCGLVCTSVNMNT 79

RESULT 5
ID 091E66 PRELIMINARY: PRT: 209 AA.
AC 091E66;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DE 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
GN ENV POLYPEPTIDE, GP41 (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF107;
RA Robertson P., Robertson D., Diamond F., Souquiere S., Maucelere P.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1."
RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
FT NON_TER 1 209
SO SEQUENCE 209 AA; 24116 MW; 91AC9BE2BE74B83 CRC64;

Query Match
Best Local Similarity 91.5%; Score 161; DB 12; Length 209;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIONQDLDMCKGRCGLVCTSVNMNT 32
DB 46 ALETLIONQDLDMCKGRCGLVCTSVNMNT 77

RESULT 6
ID 091E32 PRELIMINARY: PRT: 240 AA.
AC 091E32;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DE 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 7M GP41 (FRAGMENT).
GN ENV POLYPEPTIDE, GP41 (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF111;
RA Robertson P., Souquiere S., Diamond F., Maucelere P.,

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Page 3

Depienne C., Brun-Vezinet F., Dormont D., Simon F.O.;
Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates.
Submitted (JUN-1999) to the EMBL/Genbank/DBD databases.

DR EMBL: AJ243365; CAB9635.1; -
FT NON_TER 240 1 240
FT NON_TER 240 1 240
SEQUENCE 240 AA: 27723 MW: 1E20E8D491A197 CRC64:

Query Match 91.5%; Score 161; DB 12; Length 240;
Best Local Similarity 84.4%; Pred. No. 1.9e-16;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

1 ALETLN00LLDLMGCRGRILCTYSVKNMT 32
|||||:|||||:|||||:|||||:|||||:
50 ALETLN00LLDLMGCRGRILCTYSVKNMT 81

RESULT 7
ID 091HB8 PRELIMINARY; PRT: 125 AA.

091HB8
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN Human immunodeficiency virus type 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7676;
RA Philippe M.; Gao F., Fonjongo P.N., Zekeng L., van der Groen G.,
Pleniak D., Schable C., Lal R.B.; and transmembrane regions of HIV
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
type 1 group O." Retroviruses 16:1075-1081(2000).
RL EMBL: AF232256; AAF71913.1; -
DR EMBL: AF232256; AAF71913.1; -
FT NON_TER 125 1 125
FT NON_TER 125 1 125
SEQUENCE 125 AA: 15108 MW: E8296C4B25FF342 CRC64:

Query Match 90.9%; Score 160; DB 12; Length 125;
Best Local Similarity 81.2%; Pred. No. 1.4e-16;
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

1 ALETLN00LLDLMGCRGRILCTYSVKNMT 32
|||||:|||||:|||||:|||||:|||||:
27 ALETLN00LLDLMGCRGRILCTYSVKNMT 58

RESULT 8
ID 091EA5 PRELIMINARY; PRT: 216 AA.

091EA5
AC 091EA5: 2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENV POLYPEPTIDE (FRAGMENT).
GN Human immunodeficiency virus type 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF15;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
Philippe M.; G analysis and sub-typing of 47 HIV-1 group O isolates.*
RT Submitted (JAN-1999) to the EMBL/Genbank/DBD databases.
DR EMBL: AJ236415; CAB96263.1; -
FT NON_TER 536 1 536
FT NON_TER 536 1 536
SEQUENCE 536 AA: 60419 MW: 0F533ABN0BF552 CRC64:

Query Match 90.9%; Score 160; DB 12; Length 216;
Best Local Similarity 87.5%; Pred. No. 2.4e-16;
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 ALETLN00LLDLMGCRGRILCTYSVKNMT 32
|||||:|||||:|||||:|||||:|||||:
32 ALETLN00LLDLMGCRGRILCTYSVKNMT 63

RESULT 9
ID 091EB2 PRELIMINARY; PRT: 230 AA.

091EB2
AC 091EB2: 2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENV POLYPEPTIDE (FRAGMENT).
GN Human immunodeficiency virus type 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF15;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
Philippe M.; G analysis and sub-typing of 47 HIV-1 group O isolates.*
RT Submitted (FEB-1999) to the EMBL/Genbank/DBD databases.
DR EMBL: AJ236415; CAB96263.1; -
FT NON_TER 536 1 536
FT NON_TER 536 1 536
SEQUENCE 536 AA: 60419 MW: 0F533ABN0BF552 CRC64:

FT NON_TER 1 1
FT NON_TER 216 216
SEQUENCE 216 AA: 0A5AC18BFA88932 CRC64:

Query Match 90.9%; Score 160; DB 12; Length 216;
Best Local Similarity 87.5%; Pred. No. 2.4e-16;
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 ALETLN00LLDLMGCRGRILCTYSVKNMT 32
|||||:|||||:|||||:|||||:|||||:
32 ALETLN00LLDLMGCRGRILCTYSVKNMT 63

RESULT 9
ID 091EB2 PRELIMINARY; PRT: 230 AA.

091EB2
AC 091EB2: 2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENV POLYPEPTIDE (FRAGMENT).
GN Human immunodeficiency virus type 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF15;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
Philippe M.; G analysis and sub-typing of 47 HIV-1 group O isolates.*
RT Submitted (JAN-1999) to the EMBL/Genbank/DBD databases.
DR EMBL: AJ236415; CAB96256.1; -
FT NON_TER 230 1 230
FT NON_TER 230 1 230
SEQUENCE 230 AA: 26705 MW: C1E744FB2F51302D CRC64:

Query Match 90.9%; Score 160; DB 12; Length 230;
Best Local Similarity 84.4%; Pred. No. 1.9e-16;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 ALETLN00LLDLMGCRGRILCTYSVKNMT 32
|||||:|||||:|||||:|||||:|||||:
45 ALETLN00LLDLMGCRGRILCTYSVKNMT 76

RESULT 10
ID 091EB5 PRELIMINARY; PRT: 536 AA.

091EB5
AC 091EB5: 2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENV POLYPEPTIDE (FRAGMENT).
GN Human immunodeficiency virus type 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF15;
RA Roques P., Robertson D., Simon F., Souquiere S., Maucel P.,
Philippe M.; C phylogenetic analysis of C-gp41 region.*
RT Submitted (FEB-1999) to the EMBL/Genbank/DBD databases.
DR EMBL: AJ236415; CAB96223.1; -
FT NON_TER 536 1 536
FT NON_TER 536 1 536
SEQUENCE 536 AA: 60419 MW: 0F533ABN0BF552 CRC64:

Query Match 90.9%; Score 160; DB 12; Length 230;
Best Local Similarity 84.4%; Pred. No. 1.9e-16;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 ALETLN00LLDLMGCRGRILCTYSVKNMT 32
|||||:|||||:|||||:|||||:|||||:
45 ALETLN00LLDLMGCRGRILCTYSVKNMT 76

RESULT 10
ID 091EB5 PRELIMINARY; PRT: 536 AA.

091EB5
AC 091EB5: 2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENV POLYPEPTIDE (FRAGMENT).
GN Human immunodeficiency virus type 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF15;
RA Roques P., Robertson D., Simon F., Souquiere S., Maucel P.,
Philippe M.; C phylogenetic analysis of C-gp41 region.*
RT Submitted (FEB-1999) to the EMBL/Genbank/DBD databases.
DR EMBL: AJ236415; CAB96223.1; -
FT NON_TER 536 1 536
FT NON_TER 536 1 536
SEQUENCE 536 AA: 60419 MW: 0F533ABN0BF552 CRC64:

Query Match 90.9%; Score 160; DB 12; Length 230;
Best Local Similarity 84.4%; Pred. No. 1.9e-16;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 ALETLN00LLDLMGCRGRILCTYSVKNMT 32
|||||:|||||:|||||:|||||:|||||:
45 ALETLN00LLDLMGCRGRILCTYSVKNMT 76

Query Match
Best Local Similarity 90.9% Score 160; DB 12; Length 536;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 1 ALETLIONQOLLDMCKGRGLVCTYSVNMKT 32
DB 351 ALETLIONQOLLDMCKGRGLVCTYSVNMKT 382

RESULT 11
ID 091E09 PRELIMINARY; PRT: 544 AA.
AC 091E09; (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE ENV POLYPEPTIDE (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
RN NCBI_TaxID=11676;
RP SEQUENCE FROM N.A.
RA STRAIN=H9761;
RT Rognes P., Robertson D., Diamond F., Souquiere S., Manclere P.,
HIV-1 group O phylogenetic analysis of C2-gp41 region.
RL Submitted (FEB-1999) to EMBL/GenBank/DBJ databases.
FR EMBL: A113068; CAB96229.1;
FT NON_TER 1 544
FT SEQUENCE 544 AA: 61398 MW: FC3CPAE3IDBD50 CRC64;

Query Match
Best Local Similarity 90.9% Score 160; DB 12; Length 544;
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 1 ALETLIONQOLLDMCKGRGLVCTYSVNMKT 32
DB 360 ALETLIONQOLLDMCKGRGLVCTYSVNMKT 391

RESULT 12
ID 0A0459 PRELIMINARY; PRT: 116 AA.
AC 0A0459; (TREMblrel. 05, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE ENVELOPE TRANSMEMBRANE GP41 (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
RN NCBI_TaxID=11676;
RP SEQUENCE FROM N.A.
RA STRAIN=GROUP O.
RC Albollet-Ruho F., Ekasa R., Peeters M., Delaporte E.,
Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y09775; CAAY0914.1;
DR PPV: AF00517; GP41.1;
KM Transmembrane.1
FT NON_TER 1 116
FT SEQUENCE 116 AA: 13975 MW: 12B3DDDDZAIAD32 CRC64;

Query Match
Best Local Similarity 90.3% Score 159; DB 12; Length 116;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
OY 1 ALETLIONQOLLDMCKGRGLVCTYSVNMKT 32

DB 29 ALETLIONQOLLDMCKGRGLVCTYSVNMKT 60

RESULT 13
ID 091E05 PRELIMINARY; PRT: 137 AA.
AC 091E05; (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE ENV POLYPEPTIDE (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
RN NCBI_TaxID=11676;
RP SEQUENCE FROM N.A.
RA STRAIN=970W761;
RT Virology, Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,
Phylogenetic analysis of HIV-1 group O gp41 and transmembrane regions of HIV
*Physiologic and pathologic analysis of C2-gp41 region.
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
FR EMBL: AF229229; AAF1906.1;
FT NON_TER 1 137
FT SEQUENCE 137 AA: 16494 MW: 55C47096D816A93 CRC64;

Query Match
Best Local Similarity 90.3% Score 159; DB 12; Length 137;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
OY 1 ALETLIONQOLLDMCKGRGLVCTYSVNMKT 32
DB 30 ALETLIONQOLLDMCKGRGLVCTYSVNMKT 61

RESULT 14
ID 091E03 PRELIMINARY; PRT: 208 AA.
AC 091E03; (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE GP41 (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
RN NCBI_TaxID=11676;
RP SEQUENCE FROM N.A.
RA STRAIN=YEF32;
RC Rognes P., Robertson D., Sandline S., Christel D., Francois S.,
Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: A22641; CA96205.1;
FT NON_TER 208
FT SEQUENCE 208 AA: 24286 MW: 1C2961C35A07A1 CRC64;

Query Match
Best Local Similarity 90.3% Score 159; DB 12; Length 208;
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
OY 1 ALETLIONQOLLDMCKGRGLVCTYSVNMKT 32
DB 24 ALETLIONQOLLDMCKGRGLVCTYSVNMKT 55

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RESULT 15

ID 011942 PRELIMINARY; PRT: 342 AA.

AC 011942; 1997 (TREMBLER, 04, Created)

BT 01-JUL-1997 (TREMBLER, 04, Last sequence update)

DT 01-MAY-2000 (TREMBLER, 13, Last annotation update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Varusae; Retroviridae; Retroviridae; Lentivirus.

OK 11173xIDP11676;

RP SEQUENCE FROM N.A.

RC STRAIN-AB21561.

RA MEDLINE-97340911. PubMed-9197385.

RA Breiman C.A., Hackett L., Leopold Z., Lund J.K., Vallari A.S.,

RA Hickman S.G., Outley L., Kaplow L., von Overbeck J., Hampi H.,

RA *Sequence of gp120 immunodominant region of HIV type 1 group O from

west central Africa.*

AIDS Res. Hum. Retroviruses 13:901-904(1997).

EMBL: U90135; AB82818.1.

DR INTERPRO: I000023.

DR PROSITE: PS00577; GP11.1.

DR ENVELOPE PROTEIN.

FM NON_TER 1 1

FT NON_TER 342 342

SEQUENCE 342 AA: 38464 MW: E337FECBA29867A1 CRC64:

Query Match 90.3%; Score 159; DB 12; Length 342;

Identical Similarity 84.4%; Pred. No. 5, 4e-16; Indels 0; Gaps 0;

Matches 27; Conservative 5; Mismatches 0;

DB 1 ALETLANDQILLDMCKGKGLVCTSYKNET 32

DB 65 ALETLANDQILLDMCKGKGLVCTSYKNET 96

Search completed: March 22, 2001, 10:00:46

Job time: 525 sec

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FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 436 436 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 854 AA; 95803 MW; 2E249A94DF2DB3 CRC64;

Query Match 65.3%; Score 115; DB 1; Length 854;
Beat Local Similarity 59.4%; Pred. No. 2.9e-09;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

1 ALETLQNLQNDLLDMGCRGLCYCTSVARNMT 32
Db 572 AVERLYLDQDQLGLGMSCKKACVCTYTPWNNNS 603

RESULT 2
ENV_HV122 STANDARD; PRI: 853 AA.
AC P12487;
ID ENV_HV122
DT 01-OCT-1989 (Rel. 12, Created)
DT 03-OCT-1989 (Rel. 12, Last sequence update)
DT 13-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE
GN GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
OS Human immunodeficiency virus type 1 (223/CDC-834 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN 1]
RA Theodore T., Buckler-White A.;
RL Submitted (Nov-1989) to the HIV data bank.
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CC or send an email to license@sib-sib.ch.)

ENVL M22639; AAA4570.1;
DR HIV_ M22639; ENV82226;
DR INTERPRO: IPR000328;
DR INTERPRO: IPR000777;
DR PFAM: PF00516; GP120; 1.
DR PFM: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Polypeptide; Transmembrane;
KW Signal.
KM CHAIN 1 30
KM CHAIN 2 508
KM CHAIN 3 853
FT CHAIN BY SIMILARITY.
FT CHAIN BY SIMILARITY.
FT CHAIN BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 329 330 BY SIMILARITY.
FT DISULFID 376 415 BY SIMILARITY.
FT DISULFID 383 415 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 97043 MW; 849B0BCBAFF7008 CRC64;

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Query Match 60.2%; Score 106; DB 1; Length 853;
Beat Local Similarity 53.1%; Pred. No. 6e-08;
Matches 17; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

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1 ALETLQNLQNDLLDMGCRGLCYCTSVARNMT 32
Db 579 AVENTLQDQLGLGMSCKKACVCTYTPWNNNS 610

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RESULT 3
ENV_HV126 STANDARD; PRI: 855 AA.
ID ENV_HV126
AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE
GN GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
OS Human immunodeficiency virus type 1 (249r 6 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN 1]
RA SEQUENCE FROM N.A.
RA M22639; ENV82226;
RA M22639; ENV82226;
RA Schuchman G., Curran J., Kalyanaraman V.S., Lasky P.A.;
RA Sanchez-Pescador R.;
RT Molecular characterization of human immunodeficiency virus from
RT zaire: nucleotide sequence analysis identifies conserved and variable
RT domains in the envelope gene.*
RL Gene 52:71-82(1987).
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ENVL M22639; AAA4570.1;
DR HIV_ M22639; ENV82226;
DR HIV_ M22639; ENV82226;

```

INTERPRO: IPR000328; -
 DR INTERPRO: IPR000777; -
 DR PFM: P000516; GP120; 1.
 DR PFM: P000517; GP41; 1.
 KM Aids: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 50
 FT CHAIN 31 53
 FT DISULFID 118 207
 FT DISULFID 125 198
 FT DISULFID 130 155
 FT DISULFID 220 249
 FT DISULFID 230 241
 FT DISULFID 298 332
 FT DISULFID 378 447
 FT DISULFID 387 417
 FT CARBOHYD 129 129
 FT CARBOHYD 140 140
 FT CARBOHYD 145 145
 FT CARBOHYD 154 154
 FT CARBOHYD 158 158
 FT CARBOHYD 166 189
 FT CARBOHYD 199 199
 FT CARBOHYD 236 236
 FT CARBOHYD 243 243
 FT CARBOHYD 264 264
 FT CARBOHYD 278 278
 FT CARBOHYD 291 291
 FT CARBOHYD 327 333
 FT CARBOHYD 340 340
 FT CARBOHYD 355 355
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 398 398
 FT CARBOHYD 404 404
 FT CARBOHYD 443 443
 FT CARBOHYD 460 460
 FT CARBOHYD 461 461
 FT CARBOHYD 464 464
 FT CARBOHYD 610 610
 FT CARBOHYD 615 615
 FT CARBOHYD 624 624
 FT CARBOHYD 636 636
 FT CARBOHYD 678 678
 FT CARBOHYD 855 AA; 96971 MW; 3BA0DE239C3457 CRC64;
 SO SEQUENCE
 Query Match 60.2%; Score 106; DB 1; Length 855;
 Best Local Similarity 53.1%; Pred. No. 6.1e-08; 7; indels 0; Gaps 0;
 Matches 17; Conservative 6; Mismatches 32
 1 ALEFLTQDLIDMGCRGLVCTYSYRANET 32
 581 AVERILKQDLIGMGCRKLICTTVPANSS 612
 ID ENV_HY12 STANDARD: PRT; 843 AA.
 ENV_HY12
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR: EXTERIOR MEMBRANE
 DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41).
 GN ENV.
 OS human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 RN SHEDENCE FROM N.A.
 RP PUBMED: 91021387; PubMed:1404605;
 RX LI, Y. Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
 RA Shaw G.M.;
 RT *Complete nucleotide sequence, genome organization, and biological
 RT properties of human immunodeficiency virus type 1 in vivo: evidence
 RT for limited detectiveness and complementation.*
 RL J. Virol. 66:6587-6600(1992).
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 CC or send an email to license@isb.slb.ch).
 CC PDB: M93256; NOT ANNOTATED_CS.
 DR PIR: H44001; H44001.
 DR INTERPRO: IPR000328; -
 DR INTERPRO: IPR000777; -
 DR PFM: P000516; GP120; 1.
 DR PFM: P000517; GP41; 1.
 KM Aids: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 489
 FT CHAIN 30 843
 FT TRANSMEM 738 753
 FT DISULFID 53 73
 FT DISULFID 118 201
 FT DISULFID 130 155
 FT DISULFID 214 243
 FT DISULFID 224 235
 FT DISULFID 292 326
 FT DISULFID 373 432
 FT DISULFID 380 405
 FT CARBOHYD 87 92
 FT CARBOHYD 125 135
 FT CARBOHYD 138 138
 FT CARBOHYD 154 154
 FT CARBOHYD 158 158
 FT CARBOHYD 184 184
 FT CARBOHYD 193 193
 FT CARBOHYD 230 230
 FT CARBOHYD 236 258
 FT CARBOHYD 272 272
 FT CARBOHYD 285 285
 FT CARBOHYD 291 291
 FT CARBOHYD 297 327
 FT CARBOHYD 327 327
 FT CARBOHYD 351 381
 FT CARBOHYD 389 389
 FT CARBOHYD 395 395
 FT CARBOHYD 400 400
 FT CARBOHYD 435 435
 FT CARBOHYD 450 450
 FT CARBOHYD 458 458
 FT CARBOHYD 508 508
 FT CARBOHYD 513 612
 FT CARBOHYD 624 624
 FT CARBOHYD 803 803
 FT SEQUENCE 843 AA; 95648 MW; C69DPD71C91BB71 CRC64;
 SO SEQUENCE
 Query Match 59.7%; Score 105; DB 1; Length 843;
 Best Local Similarity 56.7%; Pred. No. 8.4e-08;

[illegible]

ET	CARBONHD	301	N-LINKED	(GLONC)	()	(POTENTIAL)
ET	CARBONHD	332	N-LINKED	(GLONC)	()	(POTENTIAL)
ET	CARBONHD	339	N-LINKED	(GLONC)	()	(POTENTIAL)
ET	CARBONHD	356	N-LINKED	(GLONC)	()	(POTENTIAL)
ET	CARBONHD	386	N-LINKED	(GLONC)	()	(POTENTIAL)
ET	CARBONHD	392	N-LINKED	(GLONC)	()	(POTENTIAL)
ET	CARBONHD	401	N-LINKED	(GLONC)	()	(POTENTIAL)
ET	CARBONHD	443	N-LINKED	(GLONC)	()	(POTENTIAL)
ET	CARBONHD	448	N-LINKED	(GLONC)	()	(POTENTIAL)
ET	CARBONHD	458	N-LINKED	(GLONC)	()	(POTENTIAL)

Query Match	Local Similarity	Score	DB 1:	Length	DB 1:
Matches	17: Conservative	56.7%	Pred. No. 8.5e-08:	7: Mismatches	0: Indels
FT	CARBOHYD	620	N-LINKED (GLC.NC)	-	(POTENTIAL)
FT	CARBOHYD	620	N-LINKED (GLC.NC)	-	(POTENTIAL)
FT	CARBOHYD	632	N-LINKED (GLC.NC)	-	(POTENTIAL)
FT	CARBOHYD	669	N-LINKED (GLC.NC)	-	(POTENTIAL)
FT	CARBOHYD	745	N-LINKED (GLC.NC)	-	(POTENTIAL)
FT	CARBOHYD	811	N-LINKED (GLC.NC)	-	(POTENTIAL)
SO	SEQUENCE	851 AA:	D1CAGC90857/935F	GR64:	

	RESULT	
OY	1 ALETLLOHNOOLDLAMGRRLGVTSYVKN 30	
	1:1 ::::1111:111:1:1:1:1	
Db	577 AVERYLKIDQDLGLTIGCSKILCTIAVPNN 606	
	ENV_HV1BN	ENV_HV1BN
ID	ENV_HV1BN	STANDARD: . PRT: 852 AA.
AC	P12468:1989 (Irel. 12, Created)	
DT	01.OCT.1989 (Irel. 12, last sequence update)	
DT	15.OCT.1989 (Irel. 38, last annotation update)	
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).	
DE	ENV.	
CN	Human immunodeficiency virus type 1 (HIV isolate) (HTV-1).	
OC	Vitruves: Retrofild Vitruves: Retroviridae: Lentivirina.	

RP SEQUENCE FROM N. A.
RX MEDLINE=69085613; PubMed=2189516;
RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Lucifora

[illegible]

[illegible]

DR HIV: K03455; ENVSH82.
 DR INTERPRO: IPR000328; -
 DR PFM: PF00516; GP120; 1.
 DR PFM: PF00517; GP41; 1.
 KW AID5: Coat protein; glycoprotein; Transmembrane;
 KW Signal.
 FT CHAIN 1 30
 FT SIGNAL 511
 FT CHAIN 512 856
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 136 196
 FT DISULFID 218 237
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 488 511
 FT CARBOHYD 138 188
 FT CARBOHYD 144 136
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 241 234
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 332 301
 FT CARBOHYD 339 336
 FT CARBOHYD 356 356
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 397 397
 FT CARBOHYD 448 406
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 634 634
 FT CARBOHYD 637 637
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 FT SEQUENCE 856 AA; 97212 MW; 67816AF85107F80 CRC64;
 Query Match
 Best Local Similarity 59.7%; Score 105; DB 1; Length 856;
 Matches 17; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
 DB 1 ALETLQNOQLDILMGCRGLACTSYVNN 30
 582 AVERLYKDDQLDLGWGSGKLTCTVANN 611
 RESULT 15
 ENV_HV1LM STANDARD: PRT: 856 AA.
 AC 070626; -
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ENVELOPE POLYPEPTIDE GP160 PROTEIN (CONTAINS: EXTERIOR MEMBRANE
 GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
 ENV.
 GN Human Immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).

OC HIV: K03455; ENVSH82.
 DR INTERPRO: IPR000328; -
 DR PFM: PF00516; GP120; 1.
 DR PFM: PF00517; GP41; 1.
 KW AID5: Coat protein; glycoprotein; Transmembrane;
 KW Signal.
 FT CHAIN 1 30
 FT SIGNAL 511
 FT CHAIN 512 856
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 136 196
 FT DISULFID 218 237
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 488 511
 FT CARBOHYD 138 188
 FT CARBOHYD 144 136
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 241 234
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 332 301
 FT CARBOHYD 339 336
 FT CARBOHYD 356 356
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 397 397
 FT CARBOHYD 448 406
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 634 634
 FT CARBOHYD 637 637
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 FT SEQUENCE 856 AA; 96938 MW; 6C41935C7E0867 CRC64;
 Query Match
 Best Local Similarity 59.7%; Score 105; DB 1; Length 856;
 Matches 17; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
 DB 1 ALETLQNOQLDILMGCRGLACTSYVNN 30
 582 AVERLYKDDQLDLGWGSGKLTCTVANN 611
 RESULT 15
 ENV_HV1LM STANDARD: PRT: 856 AA.
 AC 070626; -
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ENVELOPE POLYPEPTIDE GP160 PROTEIN (CONTAINS: EXTERIOR MEMBRANE
 GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
 ENV.
 GN Human Immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).

Matches	17;	Conservative	7;	Mismatches	6;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

QY 1 ALETLQNQLDLWCGRGLVCTSVKRN 30
.....:|:|:|

Db 582 AVERYLKDQQLGIWCCSGKLICTTAVPWN 611

Search completed: March 22, 2001, 09:57:51
Job time: 426 sec

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C:Superfamily: type E retrovirus env polypeptin

Query Match 61.4%; Score 108; DB 2; Length 358;
Best Local Similarity 60.0%; Pred. No. 1.2e-07;

Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

1 ALETLN00LDLDMGCGRLVCTSVPMN 30

DB 84 AVERLKD00LDLDMGCGRLVCTTVPMN 113

RESULT 8

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3c) (fragment

A:Species: human immunodeficiency virus type 1, HIV-1

A:Accession: S70418

A:Title: HIV-1 gp120/gp41 #sequence, revision 25-Apr-1997 #text_change 26-Aug-1999

A:Description: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro

A:Reference number: S70417; MUID:92144205

A:Accession: S70418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STR>

A:Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187

C:Superfamily: type E retrovirus env polypeptin

Query Match 61.4%; Score 108; DB 2; Length 358;
Best Local Similarity 60.0%; Pred. No. 1.2e-07;

Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

1 ALETLN00LDLDMGCGRLVCTSVPMN 30

DB 84 AVERLKD00LDLDMGCGRLVCTTVPMN 113

RESULT 9

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (fragment)

A:Species: human immunodeficiency virus type 1, HIV-1

A:Accession: S70418

A:Title: HIV-1 gp120/gp41 #sequence, revision 31-Dec-1993 #text_change 31-Jan-1997

A:Description: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92107924

A:Accession: S70418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-454 <STR>

A:Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187

C:Superfamily: type E retrovirus env polypeptin

Query Match 61.4%; Score 108; DB 2; Length 454;
Best Local Similarity 60.0%; Pred. No. 1.2e-07;

Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

1 ALETLN00LDLDMGCGRLVCTSVPMN 30

DB 84 AVERLKD00LDLDMGCGRLVCTTVPMN 113

DB 333 ALETLN00LDLDMGCGRLVCTTVPMN 362

Query Match 61.4%; Score 108; DB 2; Length 358;
Best Local Similarity 60.0%; Pred. No. 1.2e-07;

Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

1 ALETLN00LDLDMGCGRLVCTSVPMN 30

DB 84 AVERLKD00LDLDMGCGRLVCTTVPMN 113

RESULT 10

envelope protein gp120/gp41 - human immunodeficiency virus type 1

A:Species: human immunodeficiency virus type 1, HIV-1

A:Accession: S70418

A:Title: HIV-1 gp120/gp41 #sequence, revision 25-Apr-1997 #text_change 26-Aug-1999

A:Description: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144205

A:Accession: S70418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STR>

A:Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187

C:Superfamily: type E retrovirus env polypeptin

Query Match 60.8%; Score 107; DB 2; Length 358;
Best Local Similarity 60.0%; Pred. No. 1.2e-07;

Matches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

1 ALETLN00LDLDMGCGRLVCTSVPMN 30

DB 84 AVERLKD00LDLDMGCGRLVCTTVPMN 113

RESULT 11

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3b) (fragm

A:Species: human immunodeficiency virus type 1, HIV-1

A:Accession: S70417

A:Title: HIV-1 gp120/gp41 #sequence, revision 25-Apr-1997 #text_change 26-Aug-1999

A:Description: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144205

A:Accession: S70418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STR>

A:Cross-references: EMBL:X61351; NID:960184; PIDN:CAA43614.1; PID:960185

C:Superfamily: type E retrovirus env polypeptin

Query Match 60.8%; Score 107; DB 2; Length 358;
Best Local Similarity 60.0%; Pred. No. 1.2e-07;

Matches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

1 ALETLN00LDLDMGCGRLVCTSVPMN 30

DB 84 AVERLKD00LDLDMGCGRLVCTTVPMN 113

RESULT 12

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (fragment)

A:Species: human immunodeficiency virus type 1, HIV-1

A:Accession: S70418

A:Title: HIV-1 gp120/gp41 #sequence, revision 31-Dec-1993 #text_change 26-Aug-1999

A:Description: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92107924

A:Accession: S70418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-454 <STR>

A:Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187

Fri Mar 23 07:47:37 2001

us-09-147-362-13.rpt

Page 5

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Gencore version 4.5
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:52:44 ; Search time 46.96 Seconds
(without alignments)
12.236 Million cell updates/sec

Title: US-09-147-362-13

Perfect score: 176

Sequence: 1 ALETLNMDLLDMGCRNLCVTSYRNKET 32

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 174772 seqs, 17957048 residues

tal number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents-AA*
1: /cgn2_6/prodata/2/jaa/5a.comb.pep.*
2: /cgn2_6/prodata/2/jaa/5b.comb.pep.*
3: /cgn2_6/prodata/2/jaa/6.comb.pep.*
4: /cgn2_6/prodata/2/jaa/6.ctctus.comb.pep.*
5: /cgn2_6/prodata/2/jaa/backfilest.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	162	92.0	215	2	US-08-912-129A-58 Sequence 48, Appl
2	162	92.0	215	2	US-08-912-129A-58 Sequence 48, Appl
3	162	92.0	215	2	US-08-912-129A-58 Sequence 48, Appl
4	162	92.0	215	2	US-08-912-129A-58 Sequence 48, Appl
5	162	92.0	215	2	US-08-912-129A-58 Sequence 48, Appl
6	162	92.0	215	2	US-08-912-129A-58 Sequence 48, Appl
7	162	92.0	215	2	US-08-912-129A-58 Sequence 48, Appl
8	159	90.3	356	1	US-08-912-129A-61 Sequence 61, Appl
9	159	90.3	356	1	US-08-912-129A-61 Sequence 61, Appl
10	157	89.2	40	3	US-08-894-699-12 Sequence 12, Appl
11	157	89.2	40	3	US-08-894-699-12 Sequence 12, Appl
12	157	89.2	40	3	US-08-894-699-12 Sequence 12, Appl
13	157	89.2	40	3	US-08-894-699-12 Sequence 12, Appl
14	154	87.5	33	3	US-09-433-428D-10 Sequence 10, Appl
15	154	87.5	33	3	US-09-433-428D-10 Sequence 10, Appl
16	153	86.9	33	3	US-09-433-428D-15 Sequence 15, Appl
17	153	86.9	33	3	US-09-433-428D-15 Sequence 15, Appl
18	153	86.9	33	3	US-09-433-428D-15 Sequence 15, Appl
19	153	86.9	33	3	US-09-433-428D-15 Sequence 15, Appl
20	152	86.4	40	3	US-08-894-699-41 Sequence 41, Appl
21	152	86.4	40	3	US-08-894-699-41 Sequence 41, Appl
22	151	85.8	33	3	US-09-433-428D-1 Sequence 1, Appl
23	151	85.8	33	3	US-09-433-428D-1 Sequence 1, Appl
24	151	85.8	33	3	US-09-433-428D-8 Sequence 8, Appl
25	150	85.2	33	3	US-09-433-428D-23 Sequence 23, Appl
26	150	85.2	33	3	US-09-433-428D-27 Sequence 27, Appl
27	148	84.1	33	3	US-09-433-428D-13 Sequence 13, Appl
28	148	84.1	33	3	US-09-433-428D-9 Sequence 9, Appl

29	148	84.1	33	3	US-09-433-428D-14	Sequence 14, Appl
30	148	84.1	33	3	US-09-433-428D-26	Sequence 26, Appl
31	148	84.1	33	3	US-09-433-428D-29	Sequence 29, Appl
32	147	83.5	33	3	US-09-433-428D-20	Sequence 20, Appl
33	147	83.5	33	3	US-09-433-428D-25	Sequence 25, Appl
34	147	83.5	40	3	US-08-894-699-36	Sequence 36, Appl
35	147	83.5	40	3	US-08-894-699-36	Sequence 36, Appl
36	146	83.0	33	3	US-09-433-428D-61	Sequence 61, Appl
37	146	83.0	33	3	US-09-433-428D-18	Sequence 18, Appl
38	146	83.0	41	3	US-08-894-699-69	Sequence 69, Appl
39	145	82.4	33	3	US-09-433-428D-6	Sequence 6, Appl
40	145	82.4	33	3	US-09-433-428D-28	Sequence 28, Appl
41	145	82.4	33	3	US-09-433-428D-2	Sequence 2, Appl
42	145	82.4	33	3	US-09-433-428D-7	Sequence 7, Appl
43	143	81.2	33	3	US-09-433-428D-27	Sequence 27, Appl
44	143	81.2	33	3	US-09-433-428D-22	Sequence 22, Appl
45	143	81.2	33	3	US-09-433-428D-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-912-129A-58
Sequence 58, Application US/08912129A
Patent No. 5922533
INVENTOR: ANADRUZELA S.
APPLICANT: VALLART, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARTER, VINCENT A. JR.
APPLICANT: NECKLAW, ELIZABETH A.
APPLICANT: GOLDEN, ALAN RICHARD A.
APPLICANT: BRENNAN, CUSHIL G.
APPLICANT OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USN
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: MICROSOFT WORD (ASCII format output)
CURRENT APPLICATION ID: US/08/912.129A
ATTORNEY/AGENT INFORMATION:
FILING DATE: 15-AUG-1997
PRIORITY APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DANKERS, JACQUELINE M.
FIRM: ABBOTT LABORATORIES
REFERENCE/DOCKET NUMBER: 32,652
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STANDARDNESS: single
TOPOLOGY: linear
US-08-912-129A-58

Query Match 92.0%: Score 162; DB 2; Length 215;
 Best Local Similarity 84.4%: Pred. No. 1.4e-16;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ALETLNQDLDLMGCRGLVCTSVKNNET 32
 Db 117 ALETLNQDLDLMGCRGLVCTSVKNNET 148

RESULT 2
 US-08-912-129A-48
 ; Sequence 48, Application US/08912129A
 ; Patent No. 5922533
 ; GENERAL INFORMATION:
 ; APPLICANT: VALLART, ANDRUZEIA S.
 ; APPLICANT: HACKETT, JOHN JR.
 ; APPLICANT: HICKMAN, ROBERT K.
 ; APPLICANT: VARITER, VINCENT A. JR.
 ; APPLICANT: GOLDEN, ELIZABETH A.
 ; APPLICANT: BRENNAN, CATHERINE A.
 ; APPLICANT: DEVAR, SUSHL G.
 ; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
 ; NUMBER OF SEQUENCES: 89
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
 ; HARDWARE SYSTEM: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS (Windows 95)
 ; SOFTWARE: Microsoft Word (ASCII format output)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/912,129A
 ; FILING DATE: 15-AUG-1997
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Danckers, Andreas M.
 ; REGISTRATION NUMBER: 32,652
 ; REFERENCE/DOCKET NUMBER: 6109, US, 01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 847-937-9803
 ; TELEFAX: 847-938-2623
 ; INFORMATION FOR SEQ. ID NO: 48:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 245 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-912-129A-48

Query Match 92.0%: Score 162; DB 2; Length 245;
 Best Local Similarity 84.4%: Pred. No. 1.7e-16;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ALETLNQDLDLMGCRGLVCTSVKNNET 32
 Db 117 ALETLNQDLDLMGCRGLVCTSVKNNET 148

RESULT 3
 US-08-912-129A-52
 ; Sequence 52, Application US/08912129A

Patent No. 5922533.
 ; GENERAL INFORMATION:
 ; APPLICANT: VALLART, ANDRUZEIA S.
 ; APPLICANT: HACKETT, JOHN JR.
 ; APPLICANT: HICKMAN, ROBERT K.
 ; APPLICANT: VARITER, VINCENT A. JR.
 ; APPLICANT: GOLDEN, ELIZABETH A.
 ; APPLICANT: BRENNAN, CATHERINE A.
 ; APPLICANT: DEVAR, SUSHL G.
 ; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
 ; NUMBER OF SEQUENCES: 89
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
 ; HARDWARE SYSTEM: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS (Windows 95)
 ; SOFTWARE: Microsoft Word (ASCII format output)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/912,129A
 ; FILING DATE: 15-AUG-1997
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Danckers, Andreas M.
 ; REGISTRATION NUMBER: 32,652
 ; REFERENCE/DOCKET NUMBER: 6109, US, 01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 847-937-9803
 ; TELEFAX: 847-938-2623
 ; INFORMATION FOR SEQ. ID NO: 52:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 373 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-912-129A-52

Query Match 92.0%: Score 162; DB 2; Length 373;
 Best Local Similarity 84.4%: Pred. No. 2.7e-16;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ALETLNQDLDLMGCRGLVCTSVKNNET 32
 Db 117 ALETLNQDLDLMGCRGLVCTSVKNNET 148

RESULT 4
 US-08-912-129A-60
 ; Sequence 60, Application US/08912129A
 ; Patent No. 5922533
 ; GENERAL INFORMATION:
 ; APPLICANT: VALLART, ANDRUZEIA S.
 ; APPLICANT: HACKETT, JOHN JR.
 ; APPLICANT: HICKMAN, ROBERT K.
 ; APPLICANT: VARITER, VINCENT A. JR.
 ; APPLICANT: GOLDEN, ELIZABETH A.
 ; APPLICANT: BRENNAN, CATHERINE A.
 ; APPLICANT: DEVAR, SUSHL G.
 ; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
 ; NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
 COMPUTER: STEPMK IBM compatible
 OPERATING SYSTEM: MS-DOS (Windows 95)
 SOFTWARE: Microsoft Word (ASCII format output)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/912.129A
 FILING DATE: 15-AUG-1997
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Danckerts, Andreas M.
 REGISTRATION NUMBER: 32,652
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-937-9803
 TELEFAX: 847-938-2623
 INFORMATION FOR SEQ ID NO: 60:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 460 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-912.129A-60

Query Match 92.0% Score 162, DB 2, Length 460:
 Best Local Similarity 84.4% Pred. No.3, 6e-16:
 Matches 27, Conservative 5, Mismatches 0, Indels 0, Gaps 0:

DB 362 ALETLNQQLLDLMCKGRGLCYTSVKNMET 393

RESULT 5
 US-08-912.129A-50
 Sequence 50, Application US/08912129A
 Patent No.5922533
 GENERAL INFORMATION:
 APPLICANT: VALLARI, ANNARUELA S.
 APPLICANT: HACKERT, JOHN JR.
 APPLICANT: HICKMAN, ROBERT K. JR.
 APPLICANT: WALTER, VINCENT A.
 APPLICANT: GOLDEN, ALAN M.
 APPLICANT: BRENNAN, CATHERINE A.
 APPLICANT: DEYARE, SUSHIL G.
 TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
 NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS (Windows 95)
 SOFTWARE: Microsoft Word (ASCII format output)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/912.129A
 FILING DATE: 15-AUG-1997
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Danckerts, Andreas M.
 REGISTRATION NUMBER: 32,652
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-937-9803
 TELEFAX: 847-938-2623
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 490 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-912.129A-50

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/912.129A
 FILING DATE: 15-AUG-1997
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Danckerts, Andreas M.
 REGISTRATION NUMBER: 32,652
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-937-9803
 TELEFAX: 847-938-2623
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 490 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-912.129A-50

Query Match 92.0% Score 162, DB 2, Length 490:
 Best Local Similarity 84.4% Pred. No.3, 6e-16:
 Matches 27, Conservative 5, Mismatches 0, Indels 0, Gaps 0:

DB 362 ALETLNQQLLDLMCKGRGLCYTSVKNMET 393

RESULT 6
 US-08-912.129A-54
 Sequence 54, Application US/08912129A
 Patent No.5922533
 GENERAL INFORMATION:
 APPLICANT: VALLARI, ANNARUELA S.
 APPLICANT: HACKERT, JOHN JR.
 APPLICANT: HICKMAN, ROBERT K. JR.
 APPLICANT: WALTER, VINCENT A.
 APPLICANT: GOLDEN, ALAN M.
 APPLICANT: BRENNAN, CATHERINE A.
 APPLICANT: DEYARE, SUSHIL G.
 TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
 NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS (Windows 95)
 SOFTWARE: Microsoft Word (ASCII format output)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/912.129A
 FILING DATE: 15-AUG-1997
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Danckerts, Andreas M.
 REGISTRATION NUMBER: 32,652
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-937-9803
 TELEFAX: 847-938-2623
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 490 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-912.129A-54

TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
TYPE: 618 amino acids
STRANDEDNESS: 3cd
TOPOLOGY: Linear
MOLECULE TYPE: Protein
US-08-912-129A-54

Query Match
Best Local Similarity 82.0%; Score 162; DB 2; Length 618;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNOLNOLIMGCKRGILCYTSVKNMET 32
DB 362 ALETLNOLNOLIMGCKRGILCYTSVKNMET 393

RESULT 7

US-08-912-129A-61
Sequence 61, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANDRZEJ S.
APPLICANT: HICKERT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: WARTEN, ROBERT A.
APPLICANT: NEKRLANS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVAERE, SUSHIL G.
NUMBER OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
NUMBER OF SEQUENCES: 89
CORRESPONDENCES:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 5 1/4 inch diskette, 1.44 MB
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
FILING DATE: 5-AUG-1997
CLASSIFICATION NUMBER: US/08/912.129A
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dancigers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109 US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: Protein
US-08-912-129A-61

Query Match
Best Local Similarity 92.0%; Score 162; DB 2; Length 873;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNOLNOLIMGCKRGILCYTSVKNMET 32
DB 591 ALETLNOLNOLIMGCKRGILCYTSVKNMET 622

RESULT 8

US-08-602-713-12
Sequence 12, Application US/08602713
Patent No. 5798205
GENERAL INFORMATION:
APPLICANT: Hans-Peter, Knapp Stefan; Brust, Stefan;
APPLICANT: G Ritor, Luis G
APPLICANT: Zekeng, Leopold Achongbe, Joseph; Kapfue, Lazare;
TITLE OF INVENTION: Retroviruses From The HIV Group And Its Use
NUMBER OF SEQUENCES: 12
CORRESPONDENCES ADDRESS:
ADDRESSER: Knapp Stefan & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602.713
FILING DATE: 16-FEBRUARY-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 355 05 262
FILING DATE: 16-FEBRUARY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5798205man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LEDEB 203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1212 333-689200
TELEFAX: 1212 333-689112
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Protein
FRAGMENT TYPE: Internal
US-08-602-713-12

Query Match
Best Local Similarity 90.3%; Score 159; DB 1; Length 356;
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNOLNOLIMGCKRGILCYTSVKNMET 32
DB 312 ALETLNOLNOLIMGCKRGILCYTSVKNMET 343

RESULT 9

US-08-989-493-12
Sequence 12, Application US/08989493
Patent No. 6162631
GENERAL INFORMATION:
APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan;

APPLICANT: G Rtlar, Iutz G.; Eberle, Josef; Kapture, Lazare;
 APPLICANT: Zekeng, L. Opolo Achengou
 TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felle & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 Inch, 360 Kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/989,493
 FILING DATE: 01-DEC-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/602,713
 FILING DATE: 16-FEBRUARY-1996
 APPLICATION NUMBER: 08/602,762
 FILING DATE: 16-FEBRUARY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 616263man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LEADER 203
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 21212368984
 TELEFAX: 21212368984
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 356 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: Protein
 FRAGMENT TYPE: Internal
 US-08-389-435-12

Query Match 90.3%; Score 159; DB 3; Length 356;
 Best Local Similarity 81.2%; Pred. No. 7e-16; 0; Indels 0; Gaps 0;
 Matches 26; Conservative 6; Mismatches 32

1 ALETLIIONQILLDMCGRLVCYTSVKNMET 32
 DB 312 ALETLIIONQILLDMCGRLVCYTSVKNMET 343

RESULT 10
 US-08-894-699-39
 Sequence 39, Application US/08894699
 Patent No. 6030769
 GENERAL INFORMATION:
 APPLICANT: SIMON, FRANCOIS
 APPLICANT: SARAGOSTI, SENTOB
 APPLICANT: LOUSSEY-AJAKA, IBITISSAM
 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESSEE: P.C.
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 STREET: FLOOR
 CITY: ARLINGTON
 STATE: VA

COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/894,699
 FILING DATE: 01-DEC-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR96/00294
 FILING DATE: 26-FEB-1996
 APPLICATION NUMBER: FR 95/02236
 FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
 REGISTRATION NUMBER: 34,614
 REFERENCE/DOCKET NUMBER: 0354-0020-00CT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-894-699-39

Query Match 89.2%; Score 157; DB 3; Length 40;
 Best Local Similarity 84.4%; Pred. No. 1.2e-16;
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 ALETLIIONQILLDMCGRLVCYTSVKNMET 32
 DB 9 ALETLIIONQILLDMCGRLVCYTSVKNMET 40

RESULT 11
 US-08-894-699-67
 Sequence 67, Application US/08894699
 Patent No. 6030769
 GENERAL INFORMATION:
 APPLICANT: SIMON, FRANCOIS
 APPLICANT: SARAGOSTI, SENTOB
 APPLICANT: LOUSSEY-AJAKA, IBITISSAM
 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESSEE: P.C.
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 STREET: FLOOR
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/894,699
 FILING DATE: 01-DEC-1997

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR96/00294
 FILING DATE: 26-FEB-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 95/02236
 FILING DATE: 26-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,614
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 41 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 -08-894-699-67

Query Match 89.2%; Score 157; DB 3; Length 41;
 Best Local Similarity 81.2%; Pred. No. 1, 2e-16;
 Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 ALETLQNOQLDLMGCRGLVCTSVKNNST 32
 Db 9 ALETLQNOQLDLMGCRGLVCTSVKNNST 40

RESULT 12
 US-08-894-699-97
 Sequence 37; Application US/08894699
 Patent No. 6030769
 GENERAL INFORMATION:
 APPLICANT: SIMON, FRANCOIS
 APPLICANT: LOUSSEST-AJAKA, IBITISSAM
 APPLICANT: SARAGOSTI, SENIOR
 APPLICANT: LY, THOI-DUONG
 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, WATKIN & NEUSTADT,
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 STREET, FLOOR
 STATE: ARLINGTON
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 01-DEC-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR96/00294
 FILING DATE: 26-FEB-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 95/02236
 FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,614

REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-894-699-37

Query Match 89.1%; Score 155; DB 3; Length 40;
 Best Local Similarity 81.2%; Pred. No. 2, 3e-16;
 Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 ALETLQNOQLDLMGCRGLVCTSVKNNST 32
 Db 9 ALETLQNOQLDLMGCRGLVCTSVKNNST 40

RESULT 13
 US-08-894-699-42
 Sequence 42; Application US/08894699
 Patent No. 6030769
 GENERAL INFORMATION:
 APPLICANT: SIMON, FRANCOIS
 APPLICANT: LOUSSEST-AJAKA, IBITISSAM
 APPLICANT: SARAGOSTI, SENIOR
 APPLICANT: LY, THOI-DUONG
 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, WATKIN & NEUSTADT,
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 STREET, FLOOR
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 01-DEC-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR96/00294
 FILING DATE: 26-FEB-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 95/02236
 FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,614
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-894-699-42

Query Match 88.1%; Score 155; DB 3; Length 40;
Best Local Similarity 81.2%; Pred. No. 2,3e-16;
Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQQQLDLIMGCGRLCYTSVMNKT 32
DB 9 ALETLIQQQLDLIMGCGRLCYTSVMNKT 40

RESULT 14
US-09-433-428D-10
Sequence 10, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: Zheog, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 10
LENGTH: 33
TYPE: PRT
ORGANISM: Human Immunodeficiency virus type 1
US-09-433-428D-10

Query Match 87.5%; Score 154; DB 3; Length 33;
Best Local Similarity 86.7%; Pred. No. 2,6e-16;
Matches 26; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIQQQLDLIMGCGRLCYTSVMN 30
DB 4 ALETLIQQQLDLIMGCGRLCYTSVMN 33

RESULT 15
US-08-894-699-40
Sequence 40, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, PRANCIS
APPLICANT: SIMON, PRANCIS
APPLICANT: YUSSEF-AJAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/894,699
APPLICATION NUMBER: 08/894,699
FILING DATE: 01 DEC 1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 06 FEB 1996
PRIORITY DATE: 04 FEB 1996
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27 FEB 1995
ATTORNEY/AGENT INFORMATION:
NAME: OHLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0/PCT
TELECOMMUNICATIONS INFORMATION:
TELEPHONE: 703-413-1000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-40

Query Match 87.5%; Score 154; DB 3; Length 40;
Best Local Similarity 81.2%; Pred. No. 2,3e-16;
Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQQQLDLIMGCGRLCYTSVMNKT 32
DB 9 ALETLIQQQLDLIMGCGRLCYTSVMNKT 40

Search Completed: March 22, 2001, 09:52:44
Job time: 122 sec

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: March 22, 2001, 09:51:53 ; Search time 65.29 Seconds
(without alignments)
16.759 Million cell updates/sec

Title: US-09-147-362-13
Perfect score: 176
Sequence: 1 ALSTLLNQQLIDMGCRGRVYTVRNNR 32

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A. Geneseq_36.*
1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best hit being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	100.0	32	19 W80471	Peptide derived fr
2	169	95.0	32	19 W80471	Peptide derived fr
3	165	92.0	200	21 Y77373	HIV-1 group O env
4	162	92.0	215	20 Y09493	HIV-1 group O env
5	162	92.0	215	20 Y09493	Recombinant pCO-8P
6	162	92.0	215	21 Y77374	HIV-1 group O env
7	162	92.0	215	21 Y77374	HIV-1 group O env
8	162	92.0	245	20 Y09493	HIV-1 group O env
9	162	92.0	245	20 Y09493	HIV-1 group O env
10	162	92.0	245	21 Y09507	HIV-1 group O env
11	162	92.0	245	21 Y09507	HIV-1 group O env
12	162	92.0	373	20 Y09495	HIV-1 group O env

13	162	92.0	373	20 Y06979	Recombinant pCO-11
14	162	92.0	460	20 Y06980	HIV-1 group O env
15	162	92.0	460	20 Y06984	Recombinant pCO-8C
16	162	92.0	460	21 Y77375	HIV-1 group O env
17	162	92.0	474	21 Y77371	HIV-1 group O env
18	162	92.0	488	20 Y09504	HIV-1 group M and
19	162	92.0	490	20 Y09494	HIV-1 group O env
20	162	92.0	490	20 Y06978	Recombinant pCO-8C
21	162	92.0	490	21 Y06978	HIV-1 group O env
22	162	92.0	518	20 Y09495	HIV-1 group O env
23	162	92.0	618	20 Y06980	HIV-1 group O env
24	162	92.0	618	21 Y77372	HIV-1 group O env
25	162	92.0	706	20 Y09503	HIV-1 group O env
26	162	92.0	736	20 Y09501	HIV-1 group M and
27	162	92.0	873	20 Y09501	HIV-1 group M and
28	162	92.0	873	20 Y09501	Partial sequence O
29	162	92.0	873	20 Y09501	Partial sequence O
30	162	92.0	873	20 Y09501	Partial sequence O
31	162	92.0	873	20 Y09501	Partial sequence O
32	159	90.3	356	17 W03940	HIV-1 group O env
33	158	89.8	113	20 Y05546	gp 41 antigen of H
34	158	89.8	117	20 Y05546	HIV-1 group O env
35	157	89.2	40	17 W07351	Partial sequence O
36	157	89.2	41	17 W07351	Partial sequence O
37	157	89.2	715	20 Y05542	HIV-1 group O env
38	156	88.6	113	20 Y05541	HIV-1 group O env
39	156	88.6	113	20 Y05541	HIV-1 group O env
40	156	88.6	129	19 W63318	HIV-1 group O env
41	156	88.6	150	19 W63319	Anti-HIV-1 group O
42	156	88.6	150	19 W63319	Anti-HIV-1 group O
43	156	88.6	200	19 Y22908	SEB ID NO. 104 fro
44	155	88.1	40	17 W07344	Partial sequence O
45	155	88.1	40	17 W07344	Partial sequence O

ALIGNMENTS

RESULT 1
ID W80471 standard; peptide: 32 AA.
XX W80471:
XX 28-JAN-1999 (First entry)
XX
XX Peptide derived from a conserved sequence of group O human HIV.
XX
XX Group O human immune deficiency virus; HIV: detection: Infection.
XX
XX Synthetic
XX Immune deficiency virus.
XX W09845332-AL.
XX
XX 15-OCT-1998.
XX
XX 06-APR-1998; 98WO-FR00691.
XX
XX 24-SEP-1998; 98FR-0002212.
XX 09-APR-1997; 97FR-0004356.
XX
XX (SNF1) PASTEUR SANOFI DIAGNOSTICS SA.
XX Cheneboux DMB, Delagrange JFH, Gabelle SXH, Rieunier FV;
XX WPL: 1996-583190/49.
XX New synthetic peptide(s) - useful for, e.g., detecting infection by
XX human immune deficiency virus of group O
XX
XX Claim 6; Page 44; 59pp; French.
XX

CC W80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent a variable sequence
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 CC

SO Sequence 32 AA:

Query Match 100.0%; Score 176; DB 19; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1,3e-15;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLNQQLDLMGRCRLCYTSVNMET 32
 |||
 Db 1 aletllnqqlldlmgcrglrclycstvnmec 32

RESULT 2

W80470 standard; peptide; 32 AA.

W80470;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

W09845323-A1.

15-OCT-1998.

06-APR-1998; 98MC-FR00691.

24-FEB-1998; 98PR-0002212.

09-APR-1997; 97FR-0004356.

(SNF1) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

WPI: 1998-583190/49.

New synthetic peptide(s) - useful for: e.g. detecting infection by

human immune deficiency virus of group O

Claim 6; Page 44; 55pp; French.

W80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent a variable sequence
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 CC

SO Sequence 32 AA:

Query Match 96.0%; Score 169; DB 19; Length 32;
 Best Local Similarity 93.8%; Pred. No. 1,3e-15;

Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLNQQLDLMGRCRLCYTSVNMET 32
 |||
 Db 1 aletllnqqlldlmgcrglrclycstvnmec 32

RESULT 3
 W80469 standard; peptide; 32 AA.

W80469;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

W09845323-A1.

15-OCT-1998.

06-APR-1998; 98MC-FR00691.

24-FEB-1998; 98PR-0002212.

09-APR-1997; 97FR-0004356.

(SNF1) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

WPI: 1998-583190/49.

New synthetic peptide(s) - useful for: e.g. detecting infection by

human immune deficiency virus of group O

Claim 6; Page 44; 55pp; French.

W80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent a variable sequence
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 CC

SO Sequence 32 AA:

Query Match 93.8%; Score 165; DB 19; Length 32;
 Best Local Similarity 93.8%; Pred. No. 1,3e-15;

Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLNQQLDLMGRCRLCYTSVNMET 32
 |||
 Db 1 aletllnqqlldlmgcrglrclycstvnmec 32

RESULT 4

W77373 standard; Protein; 200 AA.

W77373;

22-MAY-2000 (first entry)

HIV-1 group O env gp120/gp41 pco-5 recombinant protein. SED ID NO:56.

HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;

immunoassay; positive control; affinity purification; therapeutic;

Escherichia coli; antigen; synthetic gene construction; muten;

Human immunodeficiency virus type 1 group O isolate HAM112.

Synthetic.

W0200004383-A2.

FH	Key	Location/Qualifiers
FT	Protein	2..46
ET		/note="gp120 sequence"
PT	Peptide	47..245
FM		/note="gp41 sequence"
PN	M09090410-A2.	
PD	25-FEB-1999.	
XX	07-AUG-1998;	98MO-USI6506.
PR	15-AUG-1997;	97US-0912129.
PA	(ABBO) ABBOTT LAB.	
P1	Breanan CA., Devereux SC., Golden AM., Hackett JR., Hickman RK., Neekles EC., Vallari AS., Varlick V., WPI: 1999-190224/16.	
DN	N-PDBB: X37193.	
PT	New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 - can be used in field assay; requiring no electricity and less specialised equipment	
XX	Claim 1: Fig 5; 104pp; English.	
CC	The invention relates to a rapid assay for simultaneous detection and differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The method comprises: (a) contacting the sample with a strip containing at least one immobilised capture antibody specific for HIV-1 group O, conditions sufficient to form capture reagent/capillary action, under (b) determining the presence of analyte(s) by detecting insoluble colour reagent for HIV-1 group O comprising a polypeptide shown in Y069780 and Y06981; and that for HIV-2, group M comprises a polypeptide shown in Y06982; and that for HIV-2, group N comprises a polypeptide shown in Y06981. The invention is used to screen patients for HIV-1 types O and M, and HIV-2. The invention will be particularly useful in places and situation where equipment and/or electricity is not available. The equipment provides a screening method which is faster and stable. The amino acid sequence of the recombinant pCO-8PL protein which acts as a capture reagent for HIV-1 group O.	
SO	Sequence 215 AA:	
Query Match	92.0%; Score 162; DB 20; Length 215;	
Best Local Similarity	84.4%; Pred. No: 6; 9e-14;	
Match	Conservative 27; Identities 0; Gaps 0;	
OY	1 ALETLGNOLCLDWCGRGKATCTSPNKEF 32 II7 ALELLNGQLHLHWCKRGLCYLTSYKWNET 148	
RESULT	7	
ID	Y77374	
AC	Y77374 standard; Protein, 215 AA.	
XX	Y77374;	
DE	22-MAY-2000 (first entry)	
KM	HIV-1 group O env gp120/gp41 pCO-8PL recombinant protein, SEQ ID NO:58.	
KW	Immunosay; positive control; affinity purification; therapeutic; Escherichia coli; antigen; synthetic gene construction; mutagen; deletion mutation.	

	XX	Human Immunodeficiency virus type 1 group O isolate HAM112.
OS	Synthetic.	
PM	MO200004383-A2.	
PX		
PD	27-JAN-2009.	
PF	09-JUL-1998:	96WO-US15469.
PI	14-JUL-1998:	96US-O115171.
PR	(AMBO) ABBOTT LAB.	
PT		
PS	Scheffell JM, Hackett JR, Tyner JD, Hickman RK;	
XX	WPI: 2000-171290/15.	
DR	N-PDOB: Z90285.	
DT	Newel monoclonal antibodies useful as positive control reagent for	
TX	evaluating or proposing viral disease -	
XX	Example 3; Fig 5; 14pp; English.	
CC	The invention relates to anti-HIV-1 group O monoclonal antibodies, which	
CC	may be used as positive control reagents in immunoassays to detect and	
CC	monoclonal HIV-1 infections. The invention also encompasses, detect and	
CC	which has no antibody which binds specifically to an HIV-1 group O antigen	
CC	selected from HIV-1 groups M antigens and HIV-2 antigens; and a method of	
CC	using a monoclonal antibody as	
CC	immunoassay for the detection of anti HIV-1 control reagent in an	
CC	monoclonal antibodies are useful as positive control antibodies. The	
CC	immunossays capable of detecting anti-HIV-1 group O antibodies such	
CC	antigen and develop the antigen-antibody complex. The monoclonal	
CC	provided to detect HIV-1 group O may be used to ensure that the reagents	
CC	for affinity purification of specific HIV-1 group O antibodies can be	
CC	used for generating chimeric antibodies for therapeutic use in different	
CC	epitopes of HIV antigens or purified antibodies which identify different	
CC	evaluate, or prognosticate HIV infection condition. The monoclonal	
CC	antibodies are also useful for different	
CC	from HIV-group M and HIV-2 antigens. Sequences ATGTTGGTGTTC represent	
CC	2916020266. The recombinant HIV-1 env proteins contain variable regions	
CC	recombinant HIV-1 group O antigens were purified and used to screen	
CC	hybridoma cultures.	
XO	Sequence 215 AA:	
	Query Match	97.0%; Score 162; DB 21;
	Best Local Similarity 81.4%; Pred. No. 6.9e-14;	Length 215;
	Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;	
OY	1 ALETLNNOGLLDKMGCRHVCATSTRNRNT 32	
DQ	: : : : :	
	117 atctclqngqlnlhwgcxyklycflavkwmet 148	
RESU	8	
ID	Y09493	
AC	Y09493:	
XT	15-JUN-1998 (first entry)	

DT 15-JUL-1999 (first entry)
 XX
 DE HIV-1 Group O env polypeptide p60-11pL.
 XX
 XX HIV: human immunodeficiency virus; antigen; detection; antibody;
 XX differentiation; Group O; env; immunogen; immunoassay.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 XX MO9909179-A2.
 XX
 XX 25-FEB-1999.
 XX
 XX 17-AUG-1998: 98MO-US17014.
 XX
 XX 15-AUG-1997: 97US-0911824.
 XX
 XX (ABBO) ABBOTT LAB.
 XX
 XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamauchi J:
 DR WPI: 1999-190167/16.
 XX N-PSDB: X56076.
 XX
 XX New isolated HIV-1 Group O env polypeptides - used for the
 PT detection of anti-HIV antibodies and for the production of
 XX antibodies for use in detection, purification and therapy
 XX
 PS Claim 15: Fig 9; 138pp: English.
 XX
 XX The present invention describes (1) an isolated HIV-1 Group O env
 CC polypeptide. Also described are (2) an isolated HIV-1 Group O env
 CC polypeptide comprising an immunoreactive portion of a polypeptide as in
 CC (1); (3) an antigen construct comprising a first HIV-1 Group O env polypeptide
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct
 CC comprising a fusion of a first additional HIV-1 polypeptide, a second HIV-1 env
 CC polypeptide, and at least one HIV-1 Group M env polypeptide fused to a
 CC antigen HIV-2 env polypeptide; (7) a PR encoding an antigen construct as
 CC in (3)-(6); (8) an expression vector comprising a PR as in (7); (9) an
 CC host cell transformed by an expression vector as in (8); and (10) an
 CC immunoassay kit for the detection of antibodies to HIV-1. The kit can be used for
 CC the detection of anti-HIV-1 and HIV-2 antibodies in test samples. They can also be
 CC used as immunogen for the production of antibodies. The antibodies can be used to
 CC purify polypeptides, for therapy and for detection of HIV
 CC polypeptides.
 XX
 XX Sequence 373 AA:
 SQ
 Query Match 92.0%: Score 162; DB 20; Length 373;
 Best Local Similarity 84.4%: Pred. No. 1.2e-13;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ALETTLLNOOGLDLMGCRGRVCTSVYNNET 32
 DB 117 ALETTLLNQGLINLVGCRGRVCTSVYNNET 148
 ID Y06979 standard; Protein: 373 AA.
 XX Y06979:
 AC Y06979:
 DT 06-JUL-1999 (first entry)
 XX
 XX Recombinant p60-11pL protein.
 XX

KW HIV-1: HIV-2: immobilised capture reagent; capillary action; screening;
 XX antibody; assay.
 XX
 OS Synthetic
 XX Human immunodeficiency virus type 1.
 XX
 XX Key Location/Qualifiers
 XX 2..46
 XX Protein
 XX Peptide
 XX /note="gp120 sequence"
 XX /note="gp41 sequence"
 XX
 XX MO9909410-A2.
 XX
 XX 25-FEB-1999.
 XX
 XX 07-AUG-1998: 98MO-US16506.
 XX
 XX 15-AUG-1997: 97US-0912129.
 XX
 XX (ABBO) ABBOTT LAB.
 XX
 XX Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;
 PI Necklaws EC, Waller AS, Vartick V:
 DR WPI: 1999-190224/16.
 XX N-PSDB: X37191.
 XX
 XX New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -
 PT can be used in field assay, requiring no electricity and less
 PT specialised equipment
 PT
 PS Claim 1: Fig 9; 104pp: English.
 XX
 XX The invention relates to a rapid assay for simultaneous detection and
 XX differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The
 CC method comprises (a) contacting the sample with a strip containing the sample
 CC least one immobilised capture reagent per analyte; (b) incubating the sample
 CC moves from the proximal to the distal reagent/analyte complexes, and
 CC conditions sufficient to the presence of analyte(s) by detecting a visible colour
 CC (b) determine the capture site on the strip wherein the capture
 CC reagent for HIV-1 group O comprises a polypeptide shown in Y06977-80 and
 CC Y06983-84; and that for HIV-1 group M comprises a polypeptide shown in
 CC Y06988-94; and that for HIV-2 comprises the polypeptide shown in Y06991-94
 CC M, and HIV-2. The invention is useful for antibody detection in places and
 CC situation where equal screening method which is faster and requires less
 CC equipment than prior art methods. The present sequence represents a
 CC amino acid sequence of the recombinant p60-11pL recombinant protein which
 CC acts as a capture reagent for HIV-1 group O.
 XX
 XX Sequence 373 AA:
 SQ
 Query Match 92.0%: Score 162; DB 20; Length 373;
 Best Local Similarity 84.4%: Pred. No. 1.2e-13;
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ALETTLLNOOGLDLMGCRGRVCTSVYNNET 32
 DB 117 ALETTLLNQGLINLVGCRGRVCTSVYNNET 148
 ID Y09500 standard; Protein: 460 AA.
 XX Y09500:
 AC Y09500:
 DT 15-JUL-1999 (first entry)
 XX
 XX

DE HIV-1 Group O env polypeptide pCO-8CKs.

XX HIV-1: human immunodeficiency virus; antigen: detection: antibody:
 KM differentiation: Group O; env; immunogen: immunoassay.

XX Human immunodeficiency virus type 1.

XX MO9909179-A2.

XX 25-FEB-1999.

XX 17-AUG-1998: 98MO-US17014.

XX 15-AUG-1997: 97US-0911824.

XX (ABBO) ABBOTT LAB.

XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;
 WI: 1999-190167/15.

XX N-PSDB: X35079.

PT New isolated HIV-1 Group O env polypeptides - used for the
 PT detection of anti-HIV-1 antibodies and for the production of
 PT antibodies for use in detection, purification and therapy

XX Example 3: Fig 6: 138pp: English.

XX The present invention describes (A) an isolated HIV-1 Group O env
 CC polypeptide as described are: (1) an isolated HIV-1 Group O env
 CC polypeptide comprising a nonreactive portion of a polypeptide as in
 CC (A); (2) a polynucleotide (B); (3) an antigen construct comprising a first
 CC (3) an antigen construct comprising a first HIV-1 Group O env polypeptide
 CC fused to a second HIV-1 Group O env polypeptide; (4) a polynucleotide
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at
 CC least one HIV-1 Group O env polypeptide; (5) an antigen construct
 CC comprising a fusion of a first additional HIV-1 polypeptide; (6) an
 CC antigen construct comprising a first HIV-1 polypeptide; (7) a polynucleotide
 CC in (3)-(6); (8) an expression vector comprising an antigen construct as
 CC host cell transformed by an expression vector as in (8); and (9) a
 CC antigen assay kit for the detection of antibodies to HIV-1 comprising an
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be
 CC used as immunogens to produce antibodies. The antibodies can be used to
 CC purify HIV polypeptides, for therapy and for detection of HIV
 CC polypeptides.

XX Sequence 460 AA:

XX Query Match 92.0%; Score 162; DB 20: Length 460;
 XX Best Local Similarity 84.4%; Pred. No. 1, 5e-13;

XX Matches 27: Conservative 5; Mismatches 0; Indels 0; Gaps 0;

XX 1 ALETLQNGQLDNGCRGLVCTSYRNMT 32

XX Db 362 aletlqngqlnbgcrgllyctsyvwnet 393

XX RESULT 15

XX 106984 standard: Protein: 460 AA.

XX AC Y06984;

XX 06-JUL-1999 (first entry)

XX Recombinant pCO-8CKs protein.

XX HIV-1: HIV-2: immobilised capture reagent; capillary action; screening;
 KM antibody; assay.

XX Synthetic
 OS Human immunodeficiency virus type 1.

XX Key

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

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XX Protein

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XX Protein

XX Protein

XX Protein

XX Search completed: March 22, 2001, 09:51:54
 XX Job time: 72 sec

XX Query Match 92.0%; Score 162; DB 20: Length 460;
 XX Best Local Similarity 84.4%; Pred. No. 1, 5e-13;

XX Matches 27: Conservative 5; Mismatches 0; Indels 0; Gaps 0;

XX 1 ALETLQNGQLDNGCRGLVCTSYRNMT 32

XX Db 362 aletlqngqlnbgcrgllyctsyvwnet 393

XX The invention relates to a rapid assay for simultaneous detection and
 CC differentiation of antibodies to HIV-1 groups O and M and HIV-2 -
 CC method comprises (a) contacting the sample with a strip containing the
 CC moves from immobilised capture reagent per analyte and on which the sample
 CC conditions sufficient to capture the antigen and by capillary action, under
 CC (b) determining the presence of (a) by detecting a visible colour
 CC reagent for HIV-1 group O comprises a polypeptide shown in Y06984 and
 CC Y06985-84; and that for HIV-1 group M comprises a polypeptide shown in Y06981. The
 CC M, and HIV-2. The screen patients for antibodies to HIV-1 types O and
 CC situation where equipment and/or reagent is not available. The
 CC equipment provides a screening method which is not available. The
 CC amino acid sequence of the recombinant pCO-8CKs protein which acts as a
 CC capture reagent for HIV-1 group O.

XX Sequence 460 AA:

XX Query Match 92.0%; Score 162; DB 20: Length 460;
 XX Best Local Similarity 84.4%; Pred. No. 1, 5e-13;

XX Matches 27: Conservative 5; Mismatches 0; Indels 0; Gaps 0;

XX 1 ALETLQNGQLDNGCRGLVCTSYRNMT 32

XX Db 362 aletlqngqlnbgcrgllyctsyvwnet 393

XX Search completed: March 22, 2001, 09:51:54
 XX Job time: 72 sec

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Query Match
Best Local Similarity 68.1%; Score 92; DB 2; Length 877;
Matches 15; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LN00RLNMSGCKGRKLCYTSV 22
Db 602 LN00RLNMSGCKGRKLCYTSV 623

RESULT 3

S22930
C:Species: human immunodeficiency virus type 1 (fragment)
C:Date: 06-Jun-1997 #sequence,revision 21-Jul-1995 #text_change 26-Aug-1999
R:Cooper, J.H.M.; Gueard, D.; Philibert, P.; Chameret, S.; Tabary, T.; Montagnier, L.; de
A:Description: A novel HIV-1 O strain illustrates the diversity of the O group.
A:Reference number: S52929
A:Accession: S52930
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-104 <STR>
A:Cross-references: EMBL:X84328; NID:6695526; PIDN:CAA59066.1; PID:6695527
C:Superfamily: type E retrovirus env polypeptide

Query Match
Best Local Similarity 71.3%; Score 87; DB 2; Length 104;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LN00RLNMSGCKGRKLCYTSV 22
Db 40 LN00RLNMSGCKGRKLCYTSV 61

RESULT 4

S21990
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1 HIV-1
C:Date: 20-Feb-1995 #sequence,revision 20-Feb-1995 #text_change 26-Aug-1999
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as deter
A:Reference number: S21990
A:Accession: S21990
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STR>
A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
C:Superfamily: type E retrovirus env polypeptide

Query Match
Best Local Similarity 59.1%; Score 77; DB 2; Length 357;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LN00RLNMSGCKGRKLCYTSV 22
Db 88 LN00RLNMSGCKGRKLCYTSV 109

RESULT 5

S70423
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 20) (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 20
C:Date: 19-Mar-1997 #sequence,revision 25-Apr-1997 #text_change 26-Aug-1999
R:Accession: S70423
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
A:Description: Distinct populations of human immunodeficiency virus type 1 in blood and cereb

A:Reference number: S70417; NID:92144209
A:Accession: S70423
A:Status: preliminary
A:Molecule type: RNA
A:Residues: 1-357 <STR>
A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
C:Superfamily: type E retrovirus env polypeptide

Query Match
Best Local Similarity 59.1%; Score 77; DB 2; Length 357;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LN00RLNMSGCKGRKLCYTSV 22
Db 88 LN00RLNMSGCKGRKLCYTSV 109

RESULT 6

S22002
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence,revision 20-Feb-1995 #text_change 26-Aug-1999
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete
A:Reference number: S21990
A:Accession: S22002
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STR>
A:Cross-references: EMBL:X61357; NID:960186; PIDN:CAA43616.1; PID:960187
C:Superfamily: type E retrovirus env polypeptide

Query Match
Best Local Similarity 59.1%; Score 77; DB 2; Length 358;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LN00RLNMSGCKGRKLCYTSV 22
Db 89 LN00RLNMSGCKGRKLCYTSV 110

RESULT 7

S70418
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 31) (fragm
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 31
C:Date: 19-Mar-1997 #sequence,revision 25-Apr-1997 #text_change 26-Aug-1999
R:Accession: S70418
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
A:Description: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; NID:92144209
A:Accession: S70418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STR>
A:Cross-references: EMBL:X61357; NID:960186; PIDN:CAA43616.1; PID:960187
C:Superfamily: type E retrovirus env polypeptide

Query Match
Best Local Similarity 59.1%; Score 77; DB 2; Length 358;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LN00RLNMSGCKGRKLCYTSV 22
Db 89 LN00RLNMSGCKGRKLCYTSV 110

```

RESULT 8
WUJST
env polyprotein precursor - simian immunodeficiency virus STVCPZ
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: simian immunodeficiency virus STVCPZ
A:Note: host Pan troglodytes (chimpanzee)
C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: S09983; PIDN:90239077
N:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
N:Reference number: S09983; PMID:90239077
A:Accession: S09990
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <STEP>
C:Genetics:
A:References: EMBL:K5154; NID:958866; PIDN:CAA36407.1; PID:958874
Gene: env
Superfamily: type E retrovirus env polyprotein
Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence status predicted <P1>
F:31-500/Product: coat protein gp120 status predicted <P2>
F:501-837/Domain: coat protein gp41 status predicted <P2>
F:838-853/Domain: transmembrane #status predicted <TM1>
F:854-869/Domain: transmembrane #status predicted <TM2>
F:870-881/Domain: transmembrane #status predicted <TM3>
F:882-821/Domain: transmembrane #status predicted <TM3>
F:134,140,143,154,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45
Query Match 62.3%; Score 77; DB 1; Length 854;
Best Local Similarity 54.5%; Pred. No. 0.0008;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
OY 1 LNORLNSWCKGRVCTYSV 22
DB 577 LDDQDLGIMGSGRLCTTV 598

RESULT 9
S22006
env polyprotein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C:Accession: S22000
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hecke, W.
Submitted to the EMBL Data Library, July 1991
Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determ
A:Reference number: S22000
A:Accession: S22000
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STEP>
A:Cross-references: EMBL:X61351
C:Superfamily: type E retrovirus env polyprotein
Query Match 62.3%; Score 76; DB 2; Length 358;
Best Local Similarity 59.1%; Pred. No. 0.00051;
Matches 13; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
OY 1 LNORLNSWCKGRVCTYSV 22
DB 89 LDDQDLGIMGSGRLCTTV 110

RESULT 10
S70417
env polyprotein gp120/gp41 - human immunodeficiency virus type 1 (patient 3b) (fragment
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3b
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999

```

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C:Accession: S70417
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8: 53-59 1992
C:Species: human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; PMID:92144209
A:Accession: S70417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STEP>
A:Cross-references: EMBL:X61351; NID:960194; PIDN:CAA3614.1; PID:960185
C:Superfamily: type E retrovirus env polyprotein
Query Match 62.3%; Score 76; DB 2; Length 358;
Best Local Similarity 59.1%; Pred. No. 0.00051;
Matches 13; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
OY 1 LNORLNSWCKGRVCTYSV 22
DB 89 LDDQDLGIMGSGRLCTTV 110

RESULT 11
A45713
Env transmembrane protein gp43 - human immunodeficiency virus type 2
C:Species: human immunodeficiency virus type 2, HIV-2
C:Date: 04-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
R:Bernett, S.W.; Quiroga, M.; Warner, A.; Dina, D.; Levy, J.A.
J. Virol. 67: 1006-1014, 1993
A:Title: Distinguishing features of an infectious molecular clone of the highly diver
A:Reference number: A45713; PMID:93124535
A:Accession: A45713
A:Status: preliminary; not compared with conceptual translation
A:Residues: 1-155 <BAR>
A:Molecule type: DNA
A:Experimental source: UCI
A:Note: sequence extracted from NCBI backbone (NCBI:123162)
C:Superfamily: type E retrovirus env polyprotein
Query Match 62.3%; Score 76; DB 2; Length 855;
Best Local Similarity 63.6%; Pred. No. 0.0011;
Matches 14; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
OY 1 LNORLNSWCKGRVCTYSV 22
DB 589 LKQDALNSWCAVRCRTTV 610

RESULT 12
S22006
env polyprotein gp120/gp41 - human immunodeficiency virus type 1 (patient 41)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S22006
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8: 53-59, 1992
A:Title: Distinct populations of HIV-1 in blood and cer
A:Reference number: S70417; PMID:92144209
A:Accession: S70417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STEP>
A:Cross-references: EMBL:X61354; NID:960190; PIDN:CAA3620.1; PID:960191
A:Experimental source: patient 41
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein
Query Match 60.7%; Score 74; DB 2; Length 357;
Best Local Similarity 54.5%; Pred. No. 0.001;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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OY 1 LN0QRLNSMCKGRLCYTSV 22
 DB 88 LKDDQLLGIMCGSKGLICTTIV 109

RESULT 13

S21994
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 R:Steueller, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 submitted to the EMBL Data Library, July 1991
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
 A:Reference number: S21990
 A:Accession: S21994
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <STR>
 A:Cross-references: EMBL:X61355; NID:960179; PIDN:CAAM3622.1; PID:960180
 Superfamily: type E retrovirus env polyprotein

Query Match 60.7% Score 74; DB 2; Length 357;
 Best Local Similarity 54.5% Pred. No. 0.001;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 OY 1 LN0QRLNSMCKGRLCYTSV 22
 DB 88 LKDDQLLGIMCGSKGLICTTIV 109

RESULT 14

S22004
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 R:Steueller, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 submitted to the EMBL Data Library, July 1991
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
 A:Reference number: S21990
 A:Accession: S22004
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <STR>
 A:Cross-references: EMBL:X61353; NID:960188; PIDN:CAAM3618.1; PID:960189
 Superfamily: type E retrovirus env polyprotein

Query Match 60.7% Score 74; DB 2; Length 357;
 Best Local Similarity 54.5% Pred. No. 0.001;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 OY 1 LN0QRLNSMCKGRLCYTSV 22
 DB 88 LKDDQLLGIMCGSKGLICTTIV 109

RESULT 15

S21996
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 R:Steueller, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res Hum Retroviruses 9: 23-35, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR
 A:Reference number: S70417; NUID:92144205
 A:Accession: S70422
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-357 <STR>
 A:Cross-references: EMBL:X61356; NID:960181; PIDN:CAAM3624.1; PID:91067129
 A:Experimental source: patient 27L
 A>Note: submitted to the EMBL Data Library, July 1991
 C:Superfamily: type E retrovirus env polyprotein

Query Match 60.7% Score 74; DB 2; Length 357;
 Best Local Similarity 54.5% Pred. No. 0.001;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 OY 1 LN0QRLNSMCKGRLCYTSV 22
 DB 88 LKDDQLLGIMCGSKGLICTTIV 109

Search completed: March 22, 2001, 09:53:46
 Job time: 184 sec

Fri Mar -23 07:47:41 2001

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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:52:44 ; Search time 46.96 seconds
(without alignments)

8.413 Million cell updates/sec

Title: US-09-147-362-14

Perfect score: 122

Sequence: 1.LINCOLNSMCKGRKRCVTSV 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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4: /cgm2_6/p/odata/2/1aa/5a.COMB.pep.*

5: /cgm2_6/p/odata/2/1aa/5a.COMB.pep.*

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	105	86.1	33	3	US-09-433-428D-6	Sequence 2, Appl
2	105	86.1	33	3	US-09-433-428D-29	Sequence 2, Appl
3	105	86.1	40	3	US-08-894-659-68	Sequence 39, Appl
4	105	86.1	33	3	US-09-433-428D-30	Sequence 30, Appl
5	103	84.4	40	3	US-08-894-659-36	Sequence 36, Appl
6	99	81.1	33	3	US-09-433-428D-7	Sequence 4, Appl
7	99	81.1	33	3	US-09-433-428D-15	Sequence 7, Appl
8	99	81.1	33	3	US-08-894-659-68	Sequence 63, Appl
9	99	81.1	41	3	US-08-894-659-68	Sequence 63, Appl
10	99	81.1	41	3	US-08-894-659-68	Sequence 63, Appl
11	99	81.1	41	3	US-08-894-659-68	Sequence 63, Appl
12	98	80.3	33	3	US-09-433-428D-5	Sequence 5, Appl
13	98	80.3	33	3	US-09-433-428D-16	Sequence 16, Appl
14	98	80.3	33	3	US-09-433-428D-14	Sequence 8, Appl
15	98	80.3	33	3	US-09-433-428D-29	Sequence 16, Appl
16	98	80.3	41	3	US-08-894-659-68	Sequence 63, Appl
17	98	80.3	41	3	US-08-894-659-68	Sequence 63, Appl
18	98	80.3	41	3	US-08-894-659-68	Sequence 63, Appl
19	98	80.3	41	3	US-08-894-659-68	Sequence 63, Appl
20	98	80.3	41	3	US-08-894-659-68	Sequence 63, Appl
21	98	80.3	41	3	US-08-894-659-68	Sequence 63, Appl
22	98	80.3	41	3	US-08-894-659-68	Sequence 63, Appl
23	98	80.3	41	3	US-08-894-659-68	Sequence 63, Appl
24	98	80.3	41	3	US-08-894-659-68	Sequence 63, Appl
25	97	79.5	33	3	US-09-433-428D-50	Sequence 10, Appl
26	96.5	79.1	123	3	US-09-433-428D-67	Sequence 57, Appl
27	96.5	79.1	123	3	US-09-433-428D-67	Sequence 57, Appl
28	96.5	79.1	220	3	US-09-433-428D-66	Sequence 66, Appl

29	96.5	79.1	358	3	US-09-433-428D-58	Sequence 58, Appl
30	96.2	78.7	33	3	US-09-433-428D-18	Sequence 18, Appl
31	96.2	78.7	33	3	US-09-433-428D-21	Sequence 21, Appl
32	96	78.7	33	3	US-09-433-428D-27	Sequence 27, Appl
33	96	78.7	33	3	US-09-433-428D-27	Sequence 27, Appl
34	96	78.7	40	3	US-08-894-659-40	Sequence 10, Appl
35	96	78.7	40	3	US-08-894-659-40	Sequence 10, Appl
36	95	77.9	33	3	US-09-433-428D-32	Sequence 12, Appl
37	95	77.9	33	3	US-09-433-428D-32	Sequence 12, Appl
38	95	77.9	33	3	US-09-433-428D-32	Sequence 12, Appl
39	95	77.9	33	3	US-09-433-428D-32	Sequence 12, Appl
40	95	77.9	33	3	US-09-433-428D-32	Sequence 12, Appl
41	94	77.0	33	3	US-09-433-428D-11	Sequence 11, Appl
42	94	77.0	33	3	US-09-433-428D-11	Sequence 11, Appl
43	94	77.0	33	3	US-09-433-428D-20	Sequence 20, Appl
44	94	77.0	33	3	US-09-433-428D-26	Sequence 26, Appl
45	94	77.0	40	3	US-08-894-659-41	Sequence 41, Appl

ALIGNMENTS

```

RESULT 1
US-09-433-428D-6
: Sequence 6, Application US/09433428D
: Patent No. 6149910
: APPLICANT: Zhong, Jiar
: TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
: FILE REFERENCE: CDS-207
: CURRENT APPLICATION NUMBER: US/09/433,428D
: CURRENT FILING DATE: 1999-11-04
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NOS: 1-70
: LENGTH: 33
: TYPE: PRT
: ORGANISM: Human Immunodeficiency virus type 1
US-09-433-428D-6

Query Match      86.1% Score 105, DB 3, Length 33;
Best Local Similarity 81.8%; Pred. No. 1.8e-09;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LINCOLNSMCKGRKRCVTSV 22
DB 9 IONQOLNSMCKGRKRCVTSV 30

RESULT 2
US-09-433-428D-25
: Sequence 25, Application US/09433428D
: Patent No. 6149910
: APPLICANT: Zhong, Jiar
: TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
: FILE REFERENCE: CDS-207
: CURRENT APPLICATION NUMBER: US/09/433,428D
: CURRENT FILING DATE: 1999-11-04
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NOS: 1-70
: LENGTH: 33
: TYPE: PRT
: ORGANISM: Human Immunodeficiency virus type 1
US-09-433-428D-25

Query Match      86.1% Score 105, DB 3, Length 33;
Best Local Similarity 81.8%; Pred. No. 1.8e-09;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

Matches 18: Conservative 2: Mismatches 2: Indels 0: Gaps 0:
 Oy 1 LNOGRLNSMCKGRGLVCTYSV 22
 Db 9 IONQOLNSMCKGRGLVCTYSV 30

RESULT 3

US-08-894-699-39
 : Sequence 39, Application US/08894699
 : Patent No. 6030769

GENERAL INFORMATION:
 APPLICANT: SIMON, FRANCOIS
 APPLICANT: SARAGOSTI, SENTOB
 APPLICANT: LOUSSEST-AJAKA, IBITISSAM
 APPLICANT: LY, THOI-DUONG
 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS: 81
 ADDRESS: P. C.
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/894,699
 FILING DATE: 01-DEC-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR96/00294
 FILING DATE: 26-FEB-1996
 PRIORITY APPLICATION NUMBER: FR 95/02236
 FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000

INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-894-699-39

Query Match
 Best Local Similarity 86.18: Score 105; DB 3; Length 40;
 Matched 18: Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LNOGRLNSMCKGRGLVCTYSV 22
 Db 14 IONQOLNSMCKGRGLVCTYSV 35

RESULT 4
 US-08-894-699-68
 : Sequence 68, Application US/08894699

Patent No. 6030769

GENERAL INFORMATION:
 APPLICANT: SIMON, FRANCOIS
 APPLICANT: SARAGOSTI, SENTOB
 APPLICANT: LOUSSEST-AJAKA, IBITISSAM
 APPLICANT: LY, THOI-DUONG
 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS: 81
 ADDRESS: P. C.
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/894,699
 FILING DATE: 01-DEC-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR96/00294
 FILING DATE: 26-FEB-1996
 PRIORITY APPLICATION NUMBER: FR 95/02236
 FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000

INFORMATION FOR SEQ ID NO: 68:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-894-699-68

Query Match
 Best Local Similarity 86.18: Score 105; DB 3; Length 40;
 Matches 18: Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LNOGRLNSMCKGRGLVCTYSV 22
 Db 14 IONQOLNSMCKGRGLVCTYSV 35

RESULT 5

US-09-433-4280-30
 : Sequence 30, Application US/094334280
 : Patent No. 6149910

GENERAL INFORMATION:
 APPLICANT: De Leys, Robert J.

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
 CURRENT FILING DATE: 1999-11-04
 NUMBER OF SEQ ID NOS: 70
 SOFTWARE: Patentin Ver. 2.0


```

; SEQ ID NO 30
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-30

```

Query Match	84.4%	Score 103;	DB 3;	Length 33;
Best Local Similarity	77.3%	Pred. No. 3.5e-09;		
Matches 17; Conservative	3;	Mismatches 2;	Indels 0;	Gaps 0;

RESULT 6
US-08-894-699-36
Sequence 36, Application US/08894699
Patent No. 6030769

Query Match	84.4%;	Score 103;	DB 3;	Length 40;
Best Local Similarity	77.3%;	Pred. No. 4.3e-09;		
Matches	17;	Conservative	3;	Mismatches 2;
			Indels	0;
			Gaps	0;

```
Qy 1 LNQORLNSWGCKGRVCYTSV 22
      : | : | | | | | | | : | | | | |
Db 14 IONQQLNSWGCKGRVCYTSV 35
```

```

RESULT 7
US-09-433-42BD-4
Sequence 4, Application US/09/43342BD
Patent No. 6,433,425
GENERAL INFORMATION:
APPLICANT: De Iveys, Robert J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,42BD
CURRENT FILING DATE: 11-04
PRIORITY DATE: 70
SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 4
LENGTH: 33
TYPE: PPT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-42BD-4

```

Query Match	81.1%;	Score 99;	DB 3;	Length 33;
Best Local Similarity	77.3%;	Pred. No. 1.4e-08;		
Matches 17;	Conservative	2;	Mismatches 3;	Indels 0;
				Gaps 0;

```

RESULT      8
US-09-433-428D-7
Sequence 7, Application US/09/433/428D
US-09-433-428D-7
GENERAL INFORMATION:
APPLICANT:  De Zeng, Robert J.
TITLE OF INVENTION:  PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE:  CDS-207
CURRENT APPLICATION NUMBER:  US/09/433,428D
CURRENT FILING DATE:  1999-11-04
SUBJECT CLASSIFICATION:  1301-1105
SUBJECT CLASSIFICATION:  1301-1105
SBO ID NO 7
SBO ID NO 7
LENGTH: 33
TYPE:  PR1
ORGANISM:  Human Immunodeficiency virus type 1
US-09-433-428D-7

```

Query Match	81.1%	Score 99:	DB 3:	Length 33:
Best Local Similarity:	77.3%:	Pred. No. 1.4e+08:		
Matches 17:	Conservative	2:	Mismatches 3:	Indels 0:
0y	1 LNQQRLSLMCKGCKRLCYTSY 22			
	:-:			
Db	9 IQNDQLSLMCKGCKRYCTTSY 30			

RESULT 9
 US-09-433-428D-15
 : Sequence 15 Application US/09433428D
 : INVENTOR: N. J. 482
 : GENERAL INFORMATION:
 : APPLICANT: De Leys, Robert J.
 : APPLICANT: Zheny, jin
 : TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP C
 : FILE REFERENCE: CDS-207

```

CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 33
TYPE: PRT
ORIGIN: Human Immunodeficiency virus type 1
US-09-433,428-15

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Query Match	81.18;	Score 99;	DB 3;	Length 33;
Best Local Similarity	77.38;	Pred. NO. 1.4e-08;		
Matches 17; Conservative	2;	Mismatches 3;	Indels 0;	Gaps 0

ULT 10
05-08-894-699-69

GENERAL INFORMATION: SIRON, FRANCOIS
APPLICANT: SIRON, STEPH
APPLICANT: LOUSSEST-FAUX, IBITISSAM
APPLICANT: LY, THOIAT-DUONG
TITLE OF INVENTION: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
NUMBER OF INVENTION: VIRUSES, AND USES THEREOF
CORRESPONDENCE ADDRESS: 81
ADDRESSEE: P.O.C., SPIVAX, MCGILLAND, MAIER & NEUSTADT
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
COMPUTER TYPE: P.C.
COMPUTER: IBM
OPERATING SYSTEM: COMPILATE
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/894, 699
APPLICATION DATE: 01-DEC-1997
CLASSIFICATION:

```
Query Match      81.18; Score 99; DB 3; Length 41;
Best Local Similarity 77.38; Pred. No. 1.7e-08;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

RESULT 11
US-08-894-699-66
; Sequence 66, Application US/08894699
; Patent No. 6030769

10000 INFORMATION: FRANCOIS
 10001 APPLICANT: SARACOST, SERGIO
 10002 APPLICANT: LOSSERT-ALUKA, IBITISSAM
 10003 APPLICANT: LY, THOI-DUONG
 10004 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
 10005 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
 10006 NUMBER OF SEQUENCES: 41
 10007 CORRESPONDENCE ADDRESS:
 10008 ADDRESS: P. OLM, SPYVAK, MCCLELLAND, MAYER & NEUSTADT
 10009 ADDRESS: 37-72 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 10010 STREET, FLORENCE
 10011 CITY: ARLINGTON
 10012 STATE: VA
 10013 COUNTRY: USA
 10014 COMPUTER: 2202
 10015 MEDIUM TYPE: FLOPPY, disk
 10016 OPERATING SYSTEM: IBM PC compatible
 10017 SOFTWARE: Patentin Release #1.0, Version #1.30
 10018 COMPILER: Patentin Release #1.0, Version #1.30
 10019 APPLICATION NUMBER: 08/984,600

SEQUENCE CHARACTERISTICS:					
LENGTH:	41	amino acids			
TYPE:	amino acid				
STRANDEDNESS:	single				
TOPOLGY:	linear				
MOTIF TYPE:	peptide				
S-08-894-699-69					
<hr/>					
Query Match	81.1%	Score 99,	DB 3,	Length 42:	
Best Local Similarity	77.3%;	Pred. No. 1.8e+08;			
Matches	17;	Conservative	3;	Mismatches	0;
				Gaps	0;
07	1	LNDRLNSKCGRGLCYCTSY	22		
	:	: ::	:: ::		
Ddb	14	IINDLNLINMGCRGLCYCTSY	35		

```

RESULT 12
US-09-433-428D-5
: Sequence 5, Application US/09433428D
: Patent No. 6149910
: GENERAL INFORMATION:
: APPLICANT: De Leys, Robert J.
: APPLICANT: Zheng, Jian
: TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
: FILE REFERENCE: CDS-207
: CURRENT APPLICATION NUMBER: US/09/433,428D
: CURRENT FILING DATE: 1999-11-04
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 33
: TYPE: PRT
: ORGANISM: Human Immunodeficiency virus type 1
US-09-433-428D-5

Query Match
Best Local Similarity 80.3%; Score 98; DB 3; Length 33;
Pred. No. 2e-08;
Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNOQRLLNSMCGKGRILCYTSV 22
: 1:||||| ||||| ||||| |||||
DB 9 IONQQLNLMGCKGRILCYTSV 30

RESULT 13
US-09-433-428D-8
: Sequence 8, Application US/09433428D
: Patent No. 6149910
: GENERAL INFORMATION:
: APPLICANT: De Leys, Robert J.
: APPLICANT: Zheng, Jian
: TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
: FILE REFERENCE: CDS-207
: CURRENT APPLICATION NUMBER: US/09/433,428D
: CURRENT FILING DATE: 1999-11-04
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 8
: LENGTH: 33
: TYPE: PRT
: ORGANISM: Human Immunodeficiency virus type 1
US-09-433-428D-8

Query Match
Best Local Similarity 80.3%; Score 98; DB 3; Length 33;
Pred. No. 2e-08;
Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNOQRLLNSMCGKGRILCYTSV 22
: 1:||||| ||||| ||||| |||||
DB 9 IONQQLNLMGCKGRILCYTSV 30

RESULT 14
US-09-433-428D-14
: Sequence 14, Application US/09433428D
: Patent No. 6149910
: GENERAL INFORMATION:
: APPLICANT: De Leys, Robert J.
: APPLICANT: Zheng, Jian
: TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
: FILE REFERENCE: CDS-207
: CURRENT APPLICATION NUMBER: US/09/433,428D
: CURRENT FILING DATE: 1999-11-04
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 14
: LENGTH: 33

```

```

: TYPE: PRT
: ORGANISM: Human Immunodeficiency virus type 1
US-09-433-428D-14

Query Match
Best Local Similarity 80.3%; Score 98; DB 3; Length 33;
Pred. No. 2e-08;
Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNOQRLLNSMCGKGRILCYTSV 22
: 1:||||| ||||| ||||| |||||
DB 9 IONQQLNLMGCKGRILCYTSV 30

RESULT 15
US-09-433-428D-16
: Sequence 16, Application US/09433428D
: Patent No. 6149910
: GENERAL INFORMATION:
: APPLICANT: De Leys, Robert J.
: APPLICANT: Zheng, Jian
: TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
: FILE REFERENCE: CDS-207
: CURRENT APPLICATION NUMBER: US/09/433,428D
: CURRENT FILING DATE: 1999-11-04
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 16
: LENGTH: 33
: TYPE: PRT
: ORGANISM: Human Immunodeficiency virus type 1
US-09-433-428D-16

Query Match
Best Local Similarity 80.3%; Score 98; DB 3; Length 33;
Pred. No. 2e-08;
Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNOQRLLNSMCGKGRILCYTSV 22
: 1:||||| ||||| ||||| |||||
DB 9 IONQQLNLMGCKGRILCYTSV 30

Search completed: March 22, 2001, 09:52:44
Job time: 122 sec

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Fri Mar 23 07:47:40 2001

us-09-147-362-14.rai

CC W80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent highly conserved
 CC connected around short highly conserved sequences present in
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 SO Sequence 22 AA:

Query Match 100.0%; Score 122; DB 19; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2, 4e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNQGRLNSMCKGRIVCYTSV 22
 DB 1 LNQGRLNSMCKGRIVCYTSV 22

SO Sequence 22 AA:

W80473 standard; peptide: 28 AA.
 W80473;
 28-JAN-1999 (first entry)
 Peptide derived from a conserved sequence of group O human HIV.
 Group O human immune deficiency virus; HIV; detection; infection.

Synthetic
 Immune deficiency virus.
 W09845323-A1.

15-OCT-1998.

06-APR-1998; 98MC-FR00691.

24-FEB-1998; 98FR-0002312.

09-APR-1997; 97FR-0004356.

(SWF1) PASTEUR SANOI DIAGNOSTICS SA.

Cheneboud DMB, Delagrange JFH, Gabelle SJX, Rieunier FY;

WPI: 1998-583190/49.

New synthetic peptide(s) - useful for e.g. detecting infection by
 human immune deficiency virus of group O
 Claim 6; Page 44; 55pp; French.

W80459-74 represent synthetic peptides (either linear or cyclised by
 Cys-Cys disulphide bonds). The peptides represent variable sequences
 of group O human immune deficiency virus (HIV). The peptides are
 useful as immunological reagents for detecting infection by group O
 human immune deficiency virus (HIV).

SO Sequence 28 AA:

Query Match 100.0%; Score 122; DB 19; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNQGRLNSMCKGRIVCYTSV 22
 DB 7 LNQGRLNSMCKGRIVCYTSV 28

RESULT 3
 W07346
 W07346 standard; peptide: 40 AA.

W07346;

03-JUN-1997 (first entry)

Partial sequence of gp1 from HIV-1 gp. O strain BCF07 (MAN).

Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;
 C23-env; gp1; gag; retrovirus; strain; gp120; hypervariable loop;
 immunogen; antibody.

Human immunodeficiency virus type 1.

W0627013-A1.

06-SEP-1996.

26-FEB-1996; 96MC-FR00294.

27-FEB-1995; 95FR-0002236.

(ASST-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

Chaix-Baudier ML, Lousselet-Ajaka I, Ly T, Saragosti S, Simon F;

WPI: 1996-412779/41.

N-PSDB: T44922.

New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 antibodies - useful for diagnosis, screening and typing, or as
 immunogens

Claim 12; Page 34; 71pp; French.

Human immunodeficiency virus type 1 (HIV-1) strains are currently divided
 into 2 major groups based on the nucleotide sequences of the envelope gene
 (env): group M containing sub-groups A-G, and group O containing the
 strains AN70 and WY5180. The invention relates to the discovery of
 several new strains of HIV-1 which can be placed in group O, based on the
 C23 sequences of the C23-env, gp1 and gag genes (see T44907-39 and
 W07329-64) (ESS) 1543 (BCF01) 1547 (BCF08) 1547 (BCF08) 1547 (BCF08)
 (NKO) and 1545 (BCF03) (POC). The sequence presented is the
 strain BCF07 (MAN) and corresponds to a fragment of the gp1 protein, O
 encoded by the env gene. The nucleic acids can be used to detect gp. O
 HIV-1 strains by hybridisation or (as primers) by gene amplification,
 also for screening and typing of such strains. Peptides encoded by the
 nucleic acids can be used as immunogens to raise Ab for detecting gp. O
 HIV-1.

SO Sequence 40 AA:

Query Match 86.1%; Score 105; DB 17; Length 40;
 Best Local Similarity 81.8%; Pred. No. 1.2e-08;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LNQGRLNSMCKGRIVCYTSV 22
 DB 14 LNQGRLNSMCKGRIVCYTSV 35

RESULT 4
 W07352
 W07352 standard; peptide: 40 AA.
 W07352;

PT New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 PT antibodies - useful for diagnosis, screening and typing, or as
 PT immunogens
 XX
 XX
 XX
 Claim 12: Page 33: 71pp: French.
 CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided
 CC into 2 major groups based on the nucleotide sequences of the envelope gene
 CC (env): group M containing sub-groups A-G, and group O containing the
 CC several new strains of HIV-1 which can be placed in group O, based on the
 CC partial sequences of the C23-env, gp41 and gag genes (see T44907-39 and
 CC W07329-64). The novel strains have been deposited as retroviruses CNCM
 CC (NNO) and 1545 (BCT03 (PCC)). The sequence presented here is from the
 CC strain BCF02 (PSS) and corresponds to a fragment of the gp41 protein
 CC encoded by the env gene. The nucleic acids can be used to detect gp. O
 CC HIV-1 strains by hybridisation or (as primers) by gene amplification,
 CC also for screening and typing of such strains. Peptides encoded by the
 CC nucleic acids can be used as immunogens to raise Ab for detecting gp. O
 CC HIV-1.
 SO Sequence 40 AA:
 Query Match 84.4%; Score 103; DB 17; Length 40;
 Best Local Similarity 77.3%; Pred. No. 2.3e-08;
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 DY 1 LMOORLLNSCKGRLVCTTSV 22
 DB 14 lmqqlinsgckgryqcytlav 35
 RESULT 7
 W07350 8
 W07350 standard: peptide: 42 AA.
 AC W07353:
 DT 03-JUN-1997 (first entry)
 XX
 XX Partial sequence of gp41 from HIV-1 gp. O strain BCF14.
 DE
 XX Human immunodeficiency virus type 1; HIV-1; envelop: group M; group O;
 XX C23-env; gp41; gag; retrovirus; strain: gp120; hypervariable loop;
 XX primer: hybridisation, amplification; PCR; polymerase chain reaction;
 XX immunogen: antibody.
 XX Human immunodeficiency virus type 1.
 XX W09627013-A1.
 XX
 XX 06-SEP-1996.
 XX
 XX 26-FEB-1996: 96MO-FR00294.
 XX
 XX 27-FEB-1995: 95FR-0002236.
 XX
 XX (ASST-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 XX Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;
 XX
 XX WPI: 1996-412779/41.
 DR
 XX
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 XX antibodies - useful for diagnosis, screening and typing, or as
 XX immunogens
 XX
 XX
 Claim 12: Page 46: 71pp: French.
 CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided

CC into 2 major groups based on the nucleotide sequences of the envelope gene
 CC (env): group M containing sub-groups A-G, and group O containing the
 CC strains AN770 and WP5180. The invention relates to the discovery of
 CC several new strains of HIV-1 which can be placed in group O, based on the
 CC partial sequences of the C23-env, gp41 and gag genes (see T44907-39 and
 CC W07329-64). The novel strains have been deposited as retroviruses CNCM
 CC (NNO) and 1545 (BCT03 (PCC)). The sequence presented here is from the
 CC strain BCF14 and corresponds to a fragment of the gp41 protein
 CC encoded by the env gene. The nucleic acids can be used to detect gp. O HIV-1
 CC strains by hybridisation or (as primers) by gene amplification, also for
 CC screening and typing of such strains. Peptides encoded by the nucleic
 CC acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.
 SO Sequence 41 AA:
 Query Match 81.1%; Score 99; DB 17; Length 41;
 Best Local Similarity 77.3%; Pred. No. 9e-08;
 Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 DY 1 LMOORLLNSCKGRLVCTTSV 22
 DB 14 lmqqlinsgckgryqcytlav 35
 RESULT 8
 W07350 8
 W07350 standard: peptide: 42 AA.
 AC W07350:
 DT 03-JUN-1997 (first entry)
 XX
 XX Partial sequence of gp41 from HIV-1 gp. O strain BCF09.
 DE
 XX Human immunodeficiency virus type 1; HIV-1; envelop: group M; group O;
 XX C23-env; gp41; gag; retrovirus; strain: gp120; hypervariable loop;
 XX primer: hybridisation, amplification; PCR; polymerase chain reaction;
 XX immunogen: antibody.
 XX Human immunodeficiency virus type 1.
 XX W09627013-A1.
 XX
 XX 06-SEP-1996.
 XX
 XX 26-FEB-1996: 96MO-FR00294.
 XX
 XX 27-FEB-1995: 95FR-0002236.
 XX
 XX (ASST-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 XX Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;
 XX
 XX WPI: 1996-412779/41.
 DR
 XX
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 XX antibodies - useful for diagnosis, screening and typing, or as
 XX immunogens
 XX
 XX
 Claim 12: Page 45: 71pp: French.
 CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided
 CC into 2 major groups based on the nucleotide sequences of the envelope gene
 CC (env): group M containing sub-groups A-G, and group O containing the
 CC strains AN770 and WP5180. The invention relates to the discovery of
 CC several new strains of HIV-1 which can be placed in group O, based on the
 CC partial sequences of the C23-env, gp41 and gag genes (see T44907-39 and
 CC W07329-64). The novel strains have been deposited as retroviruses CNCM
 CC (NNO) and 1545 (BCT03 (PCC)). The sequence presented here is from the

CC strain BCF09 and corresponds to a fragment of the gp41 protein encoded
CC by the env gene. The nucleic acids can be used to detect gp. O HIV-1
CC strains by hybridisation or (as primers) by gene amplification, also for
CC screening and typing of such strains. Peptides encoded by the env gene
CC acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.

XX Sequence 42 AA:

Query Match 81.1%; Score 99; DB 17; Length 42;

Best Local Similarity 77.3%; Pred. No. 9,3e-08; Mismatches 3; Indels 0; Gaps 0;

Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 LMOQRLNSMCKGRGLVCTSY 22

14 iqngqlnlwgcgrlvcyslv 35

RESULT 9

Y05555 standard; Protein: 116 AA.

Y05555;

19-JUL-1999 (first entry)

HIV-1 group O isolate 320 gp41 antigen.

HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;
vaccine; diagnosis; AIDS.

Human immunodeficiency virus type 1.

MO9904011-A2.

28-JAN-1999.

20-JUL-1998; 98MO-EP04522.

18-JUL-1997; 97EP-0870110.

(INNO-) INNOGENETICS NV.

Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;

WPI: 1999-132255/11.

N-PSDB: X25163.

New isolated HIV-1 group O strains - used to produce
polynucleotides, antigens and antibodies for use in diagnosis and in
vaccines for prevention of HIV-1 infection

Claim 3; Fig 6; 162pp; English.

The present sequence is an antigen of the gp41 protein of HIV-1
group O (Outlier) strain 320, an isolate from Richard. The
invention relates to new HIV-1 group O antigens (see Y05546-625),
and the use of these antigens, or nucleic acids encoding them (see
X25154-80), in the diagnosis and prophylaxis of AIDS. They can be
used as reagents for detecting HIV-1 group O infection and for
differentiating different types of HIV-1 group O infection.
Vaccines that provide protective immunity against HIV-1 infection, in
particular against HIV-1 group O infection, comprise at least one
HIV-1 type O antigen comprising such an antigen, a weakened or
attenuated form of an HIV-1 type O strain. The invention also relates to new
HIV-1 group O strains, mostly from patients from Cameroon and its
neighbouring countries.

Sequence 116 AA:

Query Match 81.1%; Score 99; DB 20; Length 116;

Best Local Similarity 77.3%; Pred. No. 2.6e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 LMOQRLNSMCKGRGLVCTSY 22

34 iqngqlnlwgcgrlvcyslv 55

RESULT 10

Y05548 standard; Protein: 117 AA.

Y05548;

19-JUL-1999 (first entry)

HIV-1 group O isolate FABA-PBMC gp41 antigen.

HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;
vaccine; diagnosis; AIDS.

Human immunodeficiency virus type 1.

MO9904011-A2.

28-JAN-1999.

20-JUL-1998; 98MO-EP04522.

18-JUL-1997; 97EP-0870110.

(INNO-) INNOGENETICS NV.

Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;

WPI: 1999-132255/11.

N-PSDB: X25156.

New isolated HIV-1 group O strains - used to produce
polynucleotides, antigens and antibodies for use in diagnosis and in
vaccines for prevention of HIV-1 infection

Claim 3; Fig 6; 162pp; English.

The present sequence is an antigen of the gp41 protein of HIV-1
group O (Outlier) strain FABA-PBMC, a Senegal isolate. The
invention relates to new HIV-1 group O antigens (see Y05546-625),
and the use of these antigens, or nucleic acids encoding them (see
X25154-80), in the diagnosis and prophylaxis of AIDS. They can be
used as reagents for detecting HIV-1 group O infection and for
differentiating different types of HIV-1 group O infection.
Vaccines that provide protective immunity against HIV-1 infection, in
particular against HIV-1 group O infection, comprise at least one
HIV-1 type O antigen, a nucleic acid encoding such an antigen, a
weakened or attenuated form of an HIV-1 type O strain. The invention also relates to new
HIV-1 group O strains, mostly from patients from Cameroon and its
neighbouring countries.

Sequence 117 AA:

Query Match 81.1%; Score 99; DB 20; Length 117;

Best Local Similarity 77.3%; Pred. No. 2.6e-07;

Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 LMOQRLNSMCKGRGLVCTSY 22

34 iqngqlnlwgcgrlvcyslv 55

RESULT 11

Y05625

ID Y05625 standard; Protein: 715 AA.
 AC Y05625;
 DT 19-JUL-1999 (first entry)
 XX HIV-1 group O isolate W645 envelope protein (Env).
 XX HIV-1 group O: Outlier strain; envelope protein; Env; antigen;
 XX vaccine; diagnosis: AIDS.
 KW Human immunodeficiency virus type 1.
 OS W09904011-A2.
 XX 28-JAN-1999.
 PD 20-JUL-1998; 96MO-EP04522.
 XX 18-JUL-1997; 97EP-0870110.
 XX (IMMO) INNOGENETICS NV.
 PI Delaporte E, Focsters M, Saman E, Vanden Haesevelde M;
 DR WPI: 1999-132255/11.
 DR N-PSDB: X25180.
 XX New isolated HIV-1 group O strains - used to produce
 PT p-nucleocapsid, antigen and antibodies for use in diagnosis and in
 PT vaccines for prevention of HIV-1 infection
 XX Claim 3: Fig 8A, 162pp: English.
 PS
 CC The present sequence is a partial Env polypeptide of HIV-1 group O
 CC (Outlier) virus isolate W645, as deduced from part of the genome
 CC of W645 (see X25180). The invention relates to new HIV-1 group O
 CC and the use of these envelope and nucleic acids encoding them (see
 CC X25184-80). In the diagnosis and vaccine field, these can be
 CC used as reagents for detecting HIV-1 group O infection for
 CC in particular for providing protective immunity against HIV-1 infection,
 CC in particular against HIV-1 group O infection, comprise at least
 CC a virus-1 type O antigen, a nucleic acid encoding such an antigen,
 CC a form of an HIV-1 type O strain, the invention also relates to new
 CC HIV-1 group O strains, obtained from patients from Cameroon, Gabon,
 CC Tchad, Nigeria, Senegal and Niger.
 SO Sequence 715 AA:
 Query Match 81.18; Score 99; DB 20; Length 715;
 Best Local Similarity 77.38; Fred. No. 1.9e-06;
 Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 LMOORLNSMGCKGRIVCYTSV 22
 Db 623 Iqmqqlnlwgcgrivcytsv 644
 RESULT 12
 W60470
 ID W60470 standard; peptide: 32 AA.
 AC W60470;
 XX 28-JAN-1999 (first entry)
 XX peptide derived from a conserved sequence of group O human HIV.
 XX Group O human immune deficiency virus; HIV; detection; infection.
 KW

XX
 OS Synthetic.
 OS Immune deficiency virus.
 XX W09845323-A1.
 XX 15-OCT-1998.
 PD 06-APR-1998; 98MO-FR00691.
 XX 24-FEB-1998; 98FR-0002212.
 XX 09-APR-1997; 97FR-0004356.
 PA (SNFI) PASTEUR SANOI DIAGNOSTICS SA.
 PI Cheneboux DMB, Delagrange JFM, Gabelle SX, Rieunier FY;
 DR WPI: 1998-583190/49.
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 XX Claim 6: Page 44; 55pp: French.
 PS
 CC W60459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC used as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 SO Sequence 32 AA:
 Query Match 80.38; Score 99; DB 19; Length 32;
 Best Local Similarity 77.38; Fred. No. 9.8e-08;
 Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 LMOORLNSMGCKGRIVCYTSV 22
 Db 6 Iqmqqlnlwgcgrivcytsv 27
 RESULT 13
 W07351
 ID W07351 standard; peptide: 41 AA.
 AC W07351;
 XX 03-JUN-1997 (first entry)
 XX Partial sequence of gp41 from HIV-1 gp. O strain BCF12.
 XX Human immunodeficiency virus type 1; HIV-1; envelope; group O;
 KW primer; hybridisation; amplification; PCR; polymerase chain reaction;
 KW immunogen; antibody.
 KW Human immunodeficiency virus type 1.
 OS W09627013-A1.
 XX 06-SEP-1996.
 PD 26-FEB-1996; 96MO-FR00294.
 XX 27-FEB-1995; 95FR-0002236.
 XX (ASST-) ASSISTANCE CHU LOUR HOPITALUX PARIS.
 PA (INSERM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI Chaly-Baudier M, Lousseret-Ajaka I, Ly T, Saragosti S, Simon F;
 XX

[illegible]

	FT	ET	N-LINKED (GL)
CARBOHYD	299	255	
CARBOHYD	331	331	

CARBOHYD	274	274	N-LINKED (GLCNAC. . .)	(POTENTIAL):
	274	274	N-LINKED (GLCNAC. . .)	(POTENTIAL):

• •

CARBOHYD	233	233	N-LINKED	(GLICMNC.)	(POTENTIAL).
CARBOHYD	230	268	N-LINKED	(GLICMNC.)	(POTENTIAL).
CARBOHYD	186	186	N-LINKED	(GLICMNC.)	(POTENTIAL).
CARBOHYD	159	159	N-LINKED	(GLICMNC.)	(POTENTIAL).
CARBOHYD	142	142	N-LINKED	(GLICMNC.)	(POTENTIAL).
CARBOHYD	134	134	N-LINKED	(GLICMNC.)	(POTENTIAL).
CARBOHYD	121	121	N-LINKED	(GLICMNC.)	(POTENTIAL).
CARBOHYD	113	113	N-LINKED	(GLICMNC.)	(POTENTIAL).
CARBOHYD	78	78	N-LINKED	(GLICMNC.)	(POTENTIAL).
CARBOHYD	69	69	N-LINKED	(GLICMNC.)	(POTENTIAL).
CARBOHYD	504	857	N-LINKED	(GLICMNC.)	(POTENTIAL).
CHAIN	20	503	POTENTIAL.		
SIGNAL	1	19	EXTERIOR MEMBRANE GLYCOPROTEIN.		
MIDNIGHT COAT PROTEIN			TRANSMEMBRANE GLYCOPROTEIN.		
ADHESION MOLECULES					
WATER CHANNEL					
CELL ADHESION MOLECULES					
INTERPRO:	IPR000348;	-			
INTERPRO:	IPR000777;	-			
PFAM:	PF00516; GP120; 1.				
PFAM:	PF00517; GHA1_1.				

[illegible]

[illegible]

```

      FT CARBOHYD    398   388   N-LINKED (GLCNAc . .) (POTENTIAL).
      FT CARBOHYD    401   401   N-LINKED (GLCNAc . .) (POTENTIAL).
      FT CARBOHYD    438   438   N-LINKED (GLCNAc . .) (POTENTIAL).
      FT CARBOHYD    454   454   N-LINKED (GLCNAc . .) (POTENTIAL).
      FT CARBOHYD    602   602   N-LINKED (GLCNAc . .) (POTENTIAL).
      FT CARBOHYD    607   607   N-LINKED (GLCNAc . .) (POTENTIAL).
      FT CARBOHYD    618   618   N-LINKED (GLCNAc . .) (POTENTIAL).
      FT CARBOHYD    628   628   N-LINKED (GLCNAc . .) (POTENTIAL).
SQ     SEQUENCE      847 AA;  96135 MW;  DA09131FD7FEC2AB CRC64;

Best Local Match              60.7%; Score 74; DB 1; Length 847;
Sequence Similarity           54.5%; Pred. No. 0.0005;
Matches 12; Conservative      4; Mismatches 6; Indels 0; Gaps 0

QY       1 LNDORILNSNGCRALVCTYSV 22
          I : I I   I I I I I : I : I
Db        578 LKDDQLGSLGSGRLICITAV 599

RESULT = 5
ENV_HIV1?
AC P05880; STANDARD; PRT; 847 AA.
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DE 15-JUL-1993 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE gp160 PRECURSOR [CONTRAINS: EXTENIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN
RS SEQUENCE FROM N.A.
RX MEDLINE=66235450; Pubmed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT *Genetic variation in HIV-II/LAV over time in patients with AIDS or
```


[illegible]

Query Match	Similarity	Score	74:	DB 1:	Length	852:
Seq. Local	12:	Conservative	4:	Mismatches	6:	Indels
Matches						Gaps
1	LN00RLINMGCGRGRLVCYVS 22	54.7%				
583	LKD0LLGIGCGSGKLICTTAV 604	54.58%				
DB	583 LKD0LLGIGCGSGKLICTTAV 604					
RESULT 8						
ENV_HYJIS3	STANDARD;					852 AA.
ENV_HYJIS3						
AD						
AD	P19549:					
DT	01-FEB-1991 (Rel. 17, Created)					
DT	01-FEB-1991 (Rel. 17, Last sequence update)					
DT	15-JUL-1999 (Rel. 38, Last annotation update)					
DE	ENVELOPE POLYPROTEIN GP160 PRECURSOR (CONVANS: EXTERIOR MEMBRANE					
GN	GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41))					
DE	ENV.					
GN	Human Immunodeficiency virus type 1 (SP3 isolate) (HIV-1).					
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.					
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.					
RE	SEQUENCE FROM N.A.					
RE	MEDLINE=90317906; PubMed=2370888;					
RA	*York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;					
RA	Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of					
RT	the viral genome.					
RL	J. Virol. 64:4016-4020(1990).					
CC	This SWISS-Prot entry is copyright. It is produced through a collaboration					
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CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/					
CC	or send an email to license@sdb.ch).					
CC	SWISS: M38427; AAA45067.1;					
CC	SWISS: M38427; AAA45067.1;					
DR	INTERPRO: IPR000328; .					

FT CARBOHYD 184 184 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 190 190 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 233 233 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 244 244 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 245 245 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 272 272 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 298 298 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 304 304 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 334 334 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 341 341 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 358 358 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 408 408 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 610 610 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 636 636 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 815 815 N-LINKED (GLCNAC . . .) (POTENTIAL).
 SQ SEQUENCE 855 AA: 97438 MW: A3BC20573AAC41A2 CRC64:

Query Match 60.74: Score 74: DB 1: Length 855:
 Best Local Similarity 54.58: Prd NO 0.0005: 4: Mismatches 6: Indels 0: Gaps 0:

QY 1 LNOQRLNSMCKGRVLCYSV 22
 DB 586 LKDDQLGJMGCSKILCTTAV 607

RESULT 12
 ENV_HY10Y STANDARD: PRT: 855 AA.
 ID ENV_HY10Y
 DT 020888: 991 (rel. 17: Created)
 DT 01-FEB-1991 (rel. 17: Last sequence update)
 DT 15-JUL-1999 (rel. 38: Last sequence update)
 DE ENVELOPE POLYPROTEIN GP160 PROCESSIONS: EXTERIOR MEMBRANE
 DE GLYCOPROTEIN (GP120): TRANSMEMBRANE GLYCOPROTEIN (GP41).
 ENV.

Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).
 [Virus]: Retroid viruses; Retroviridae; Lentivirus.

RA SEQUENCE FROM N.A.
 RA MEDLINE-90148544: Pubmed-2559749:
 RA Hueb T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.:
 "A highly defective HIV-1 strain isolated from a healthy ghanese
 AIDS 3:707-715(1989)."
 -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
 HEALTHY GHANESE INDIVIDUAL.

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 CC -----end an email to license@sib-sib.ch-----

DR EMBL: M26727: AAA8197.1: -
 DR HIV: M26727: ENV30Y: -
 DR INTERPRO: IP000328: -
 DR INTERPRO: IP000777: -
 DR EFM: P00516: GP120: 1.

DR PFAM: P00517: GP41: 1
 KW A10S: Coat protein; polyprotein; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 509
 FT DISULFID 510 895
 FT DISULFID 118 273
 FT DISULFID 135 201
 FT DISULFID 150 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 335
 FT DISULFID 388 442
 FT DISULFID 388 442
 FT CARBOHYD 134 134
 FT CARBOHYD 142 142
 FT CARBOHYD 145 145
 FT CARBOHYD 161 161
 FT CARBOHYD 165 165
 FT CARBOHYD 202 202
 FT CARBOHYD 239 239
 FT CARBOHYD 246 246
 FT CARBOHYD 267 267
 FT CARBOHYD 281 281
 FT CARBOHYD 294 294
 FT CARBOHYD 300 300
 FT CARBOHYD 306 306
 FT CARBOHYD 336 336
 FT CARBOHYD 359 359
 FT CARBOHYD 389 389
 FT CARBOHYD 395 395
 FT CARBOHYD 399 399
 FT CARBOHYD 405 405
 FT CARBOHYD 410 410
 FT CARBOHYD 610 610
 FT CARBOHYD 615 615
 FT CARBOHYD 624 624
 FT CARBOHYD 636 636
 FT CARBOHYD 815 815
 SQ SEQUENCE 855 AA: 97476 MW: 9CFB2A607AD062DA CRC64:
 Query Match 60.74: Score 74: DB 1: Length 855:
 Best Local Similarity 54.58: Prd NO 0.0005: 4: Mismatches 6: Indels 0: Gaps 0:

QY 1 LNOQRLNSMCKGRVLCYSV 22
 DB 586 LKDDQLGJMGCSKILCTTAV 607

ENV_HY126 STANDARD: PRT: 855 AA.

RESULT 13
 ID ENV_HY126
 DT 13-AUG-1987 (rel. 05: Created)
 DT 15-JUL-1999 (rel. 95: Last sequence update)
 DE ENVELOPE POLYPROTEIN GP160 PROCESSIONS: EXTERIOR MEMBRANE
 DE GLYCOPROTEIN (GP120): TRANSMEMBRANE GLYCOPROTEIN (GP41).
 ENV.

Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
 [Virus]: Retroid viruses; Retroviridae; Lentivirus.

RA SEQUENCE FROM N.A. Pubmed-303660:
 RA MEDLINE-47248097: Bangalore P., Peorlino P.,
 RA Sriyanesan A., Anand R., York
 RA Schochetman G., Curran J., Kalaynarayan V.S., Luciw P.A.,
 RA Sanchez-Pescador R.:
 *Molecular characterization of human immunodeficiency virus from

Query Match	60.7%	Score 74:	DB 1:	length 855;
Best Local Similarity	54.5%	Pred. No.	0.0005;	
Matches 12:	Conservative	4:	Mismatches	6:
			Indels	0:
			Gaps	0:
QY	1	LNQORLNSGCKRCRCVYTSV	22	

FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	160	160	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	197	197	N-LINKED (GLCNAC. . .)

[illegible]

FT	CARBOND	230	N-LINKED	(GLCANC. .)	(POTENTIAL)
FT	CARBOND	230	N-LINKED	(GLCANC. .)	(POTENTIAL)
FT	CARBOND	234	N-LINKED	(GLCANC. .)	(POTENTIAL)
FT	CARBOND	241	N-LINKED	(GLCANC. .)	(POTENTIAL)
FT	CARBOND	262	N-LINKED	(GLCANC. .)	(POTENTIAL)
FT	CARBOND	276	N-LINKED	(GLCANC. .)	(POTENTIAL)
FT	CARBOND	289	N-LINKED	(GLCANC. .)	(POTENTIAL)
FT	CARBOND	295	N-LINKED	(GLCANC. .)	(POTENTIAL)
FT	CARBOND	301	N-LINKED	(GLCANC. .)	(POTENTIAL)

FT	CARBOND	339	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	339	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	356	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	386	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	392	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	397	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	406	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	448	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	453	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	461	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	616	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	624	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	637	N-LINKED	(GLYCANC..)	(POTENTIAL)
FT	CARBOND	674	N-LINKED	(GLYCANC..)	(POTENTIAL)

Query Match	60.7%	Score 74:	DR 1:	Length 856:
Best Local Similarity	54.5%	Prod.	0.0005:	
Matches 12: Conservative	4:	Mismatches	6:	Indels
				0:
FT CARBOND	750	750	N-LINKED (GICGAC...)	(POTENTIAL)
PEP CARBOND	816	816	N-LINKED (GICGAC...)	(POTENTIAL)
SEQUENCE	856 AA:	97212 MM:	65M616M9B5107E0	CRC64:

```

1 LNOQRLINSGCKGALCYTSV 22
1 : : : : : : : : : : : :
587 LNOQRLGSLGCSGNLICTTAV 608

```

Search completed: March 22, 2001, 09:57:52
Job time: 427 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 10:00:47 : Search time 171.82 Seconds
(without alignments)
19,100 Million cell updates/sec

Title: US-09-147-362-15

Perfect score: 149

Sequence: 1 LALETLNQQRLNSGCKGRVCTSV 28

Scoring table: BLOSUM62

Gap: 10.0, Expect 0.5

Searched: 374700 seqs, 117207915 residues

Final number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-protist:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the hit. The result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	127	88.2	216	12	091EC5	091EC5 human immun
2	127	88.2	216	12	091EB5	091EB5 human immun
3	127	88.2	216	12	091EB8	091EB8 human immun
4	124	83.2	219	12	091EB8	091EB8 human immun
5	123	82.6	242	12	091EB3	091EB3 human immun
6	122	81.9	216	12	091EB5	091EB5 human immun
7	122	81.9	544	12	091EB9	091EB9 human immun
8	121	81.2	116	12	044E59	044E59 human immun
9	121	81.2	118	12	091EB5	091EB5 human immun
10	121	81.2	131	12	091EB5	091EB5 human immun
11	121	81.2	131	12	091EB5	091EB5 human immun
12	121	81.2	137	12	091EB5	091EB5 human immun
13	121	81.2	213	12	091EB3	091EB3 human immun
14	121	81.2	342	12	091EB9	091EB9 human immun
15	121	81.2	352	12	091EB9	091EB9 human immun
16	121	81.2	871	12	057072	057072 human immun
17	121	81.2	872	12	057072	057072 human immun
18	121	81.2	900	12	090N88	090N88 human immun

20	120	80.5	114	12	040448	040448 human immun
21	120	80.5	116	12	040458	040458 human immun
22	120	80.5	117	12	090EF2	090EF2 human immun
23	120	80.5	124	12	091HU7	091HU7 human immun
24	120	80.5	132	12	091HU7	091HU7 human immun
25	120	80.5	132	12	091HU4	091HU4 human immun
26	120	80.5	134	12	091HU4	091HU4 human immun
27	120	80.5	172	12	091EB3	091EB3 human immun
28	120	80.5	183	12	091EB3	091EB3 human immun
29	120	80.5	200	12	091EB7	091EB7 human immun
30	120	80.5	213	12	091EB7	091EB7 human immun
31	120	80.5	220	12	091EB7	091EB7 human immun
32	120	80.5	234	12	091EB2	091EB2 human immun
33	120	80.5	512	12	091EB2	091EB2 human immun
34	120	80.5	517	12	091EB7	091EB7 human immun
35	120	80.5	532	12	091EB7	091EB7 human immun
36	120	80.5	547	12	091EB7	091EB7 human immun
37	120	80.5	547	12	091EB7	091EB7 human immun
38	120	80.5	111	12	040452	040452 human immun
39	119	79.9	114	12	040456	040456 human immun
40	119	79.9	114	12	040457	040457 human immun
41	119	79.9	114	12	040472	040472 human immun
42	119	79.9	143	12	091RV4	091RV4 human immun
43	119	79.9	218	12	091EB5	091EB5 human immun
44	119	79.9	224	12	091EB8	091EB8 human immun

ALIGNMENTS

RESULT 1	091EC5	PRELIMINARY:	PRT:	216 AA.
ID	091EC5	PRELIMINARY:	PRT:	216 AA.
AC	091EC5	PRELIMINARY:	PRT:	216 AA.
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	GP41 (FRAGMENT).			
GN	ENV.			
OS	Human immunodeficiency virus type 1			
OC	Viruses; Retrov. viruses; Retroviridae; Lentivirus.			
OX	111			
NP	111			
RP	SEQUENCE FROM N.A.			
RC	STRAT-BCF07.			
RA	Rogues P., Robertson D., Sandline S., Christel D., Francois S., Philippe M.,			
RT	Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.			
RL	Submitted (JAN-1998) to the EMBL/Genbank/DBS databases.			
DR	KHML: A0236394; CAB9049.1.			
FT	NON-TER			
SO	SEQUENCE	216 AA:	25027 MW:	413AE9BBF1B4FC9A CRC64:
Query Match	85.2%	Score 127:	DB 12:	Length 216:
Best Local Similarity	85.2%	Score 127:	DB 12:	Length 216:
Matches	23:	Conservative	2:	Mismatches
OY	2	ALETLNOQRLNSGCKGRVCTSV 28		
DB	37	ALETLNOQRLNSGCKGRVCTSV 63		
RESULT 2	091EB6	PRELIMINARY:	PRT:	219 AA.
AC	091EB6	PRELIMINARY:	PRT:	219 AA.
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	GP41 (FRAGMENT).			

GN ENV.
OS Human Immunodeficiency Virus type 1.
OC Viruses; Retroviridae; Lentivirus.
RA NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF4.
RA Riquenes P., Robertson D., Sandrine S., Christel D., Francois S.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ236404; CAB96252.1;
FT NON-TER
FT 219 1
FT 219 1
SO SEQUENCE 219 AA; 25353 MW; F65829EB01520D91 CRC64;

Query Match
Best Local Similarity 85.2%; Score 127; DB 12; Length 219;
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 2 ALETLNODRLNSMCKGKRLVCTSV 28
DB 47 ALETLNODRLNSMCKGKRLVCTSV 73

RESULT 3
ID O9IEC3 PRELIMINARY; PRT: 219 AA.
AC O9IEC3
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Lentivirus.
RA NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF02;
RA Riquenes P., Robertson D., Sandrine S., Christel D., Francois S.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ236392; CAB96240.1;
FT NON-TER
FT 219 1
FT 219 1
SO SEQUENCE 219 AA; 25363 MW; 85CD2C5B5F328907 CRC64;

Query Match
Best Local Similarity 83.9%; Score 125; DB 12; Length 219;
Matches 22; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 2 ALETLNODRLNSMCKGKRLVCTSV 28
DB 46 ALETLNODRLNSMCKGKRLVCTSV 72

RESULT 4
ID O9IHU9 PRELIMINARY; PRT: 130 AA.
AC O9IHU9
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Lentivirus.
RA NCBI_TaxID=11676;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=97GN798;
RA Yang C., Gao F., Ponjungo P.N., Zekeng L., van der Groen G.,
RN Pieniazek D., Schable C., Lal R.B.,
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
proteins from HIV-1 isolates." *Journal of Virology* 16:1075-1081 (2000).
DR EMBL: AF229235; AAF71912.1;
FT NON-TER
FT 130 1
FT 130 1
SO SEQUENCE 130 AA; 15593 MW; 5385789A36344E4 CRC64;

Query Match
Best Local Similarity 81.2%; Score 124; DB 12; Length 130;
Matches 22; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 2 ALETLNODRLNSMCKGKRLVCTSV 28
DB 30 ALETLNODRLNSMCKGKRLVCTSV 56

RESULT 5
ID O9IE31 PRELIMINARY; PRT: 242 AA.
AC O9IE31
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE TM, GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Lentivirus.
RA NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF12;
RA Riquenes P., Robertson D., Souquiere S., Diamond F., Nauciere P.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ243366; CAB96336.1;
FT NON-TER
FT 242 1
FT 242 1
SO SEQUENCE 242 AA; 27539 MW; DEBA73DF08BA6FD7 CRC64;

Query Match
Best Local Similarity 82.6%; Score 123; DB 12; Length 242;
Matches 21; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 2 ALETLNODRLNSMCKGKRLVCTSV 28
DB 54 ALETLNODRLNSMCKGKRLVCTSV 80

RESULT 6
ID O9IEA5 PRELIMINARY; PRT: 216 AA.
AC O9IEA5
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Lentivirus.
RA NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YB2E;
RA Riquenes P., Robertson D., Sandrine S., Christel D., Francois S.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ243366; CAB96336.1;
FT NON-TER
FT 216 1
FT 216 1
SO SEQUENCE 216 AA; 25353 MW; F65829EB01520D91 CRC64;

RT: "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
 RI: Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ236415; CAB96283.1; -
 FT NON_TER 1 1
 FT NON_TER 216 216
 SO SEQUENCE 216 AA: 25003 MW: 0A5AC218BFA8932 CRC64:

Query Match 81.9% Score 122; DB 12; Length 216;
 Best Local Similarity 78.6% Pred. No. 4,56-11;
 Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RALETLNMOQLNMGCKGRVCTYSV 28
 DB 31 QALETLNMOQLNMGCKGRVCTYSV 58

RESULT 7
 OYIED9 PRELIMINARY: PRT: 544 AA.

OYIED9 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).
 OS HIV POLYMERASE (FRAGMENT).
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HIV26;
 RA Desrosiers C., Robertson D., Diamond P., Souquiere S., Maucelere P.,
 RA Desrosiers C., Brun-Vezinet F., Dormont D.;
 RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."
 RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RI EMBL: AJ133068; CAB96229.1; -
 DR EMBL: AJ133068; CAB96229.1; -
 FT NON_TER 544 544
 FT NON_TER 544 544
 SO SEQUENCE 544 AA: 61398 MW: FC3GFA4E1DE6D50 CRC64:

Query Match 81.9% Score 122; DB 12; Length 544;
 Best Local Similarity 78.6% Pred. No. 1,1e-10;
 Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RALETLNMOQLNMGCKGRVCTYSV 28
 DB 359 QALETLNMOQLNMGCKGRVCTYSV 386

RESULT 8
 OY40459 PRELIMINARY: PRT: 116 AA.

OY40459 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GROUP O;
 RA Bitbollet-Ruche F., Ekasa E., Peeters M., Delaporte E.;
 RA Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RI EMBL: Y09775; CAAT0914.1; -
 DR INTERPRO: IPR000328; -
 DR PFAM: PF00517; GP41; 1.
 KW Transmembrane protein.
 FT NON_TER 1 1
 FT NON_TER 116 116
 SO SEQUENCE 116 AA: 15736 MW: 1053F85345F8B98 CRC64:

SO SEQUENCE 116 AA: 13975 MW: 12B3D0DDDA1AD32 CRC64:

Query Match 81.2% Score 121; DB 12; Length 116;
 Best Local Similarity 81.5% Pred. No. 3,5e-11;
 Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNMOQLNMGCKGRVCTYSV 28
 DB 29 ALETLNMOQLNMGCKGRVCTYSV 55

RESULT 9
 OY40451 PRELIMINARY: PRT: 118 AA.

OY40451 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GROUP O;
 RA Bitbollet-Ruche F., Ekasa E., Peeters M., Delaporte E.;
 RA Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RI EMBL: Y09775; CAAT0918.1; -
 DR INTERPRO: IPR000328; -
 DR PFAM: PF00517; GP41; 1.
 KW Transmembrane protein.
 FT NON_TER 1 1
 FT NON_TER 118 118
 SO SEQUENCE 118 AA: 14094 MW: C4491740918DE154 CRC64:

Query Match 81.2% Score 121; DB 12; Length 118;
 Best Local Similarity 81.5% Pred. No. 3,5e-11;
 Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNMOQLNMGCKGRVCTYSV 28
 DB 29 ALETLNMOQLNMGCKGRVCTYSV 55

RESULT 10
 OY9R05 PRELIMINARY: PRT: 131 AA.

OY9R05 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 OS HIV POLYMERASE (FRAGMENT).
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=302.02;
 RA Plestiaek D., Yang C., Lai R.T.;
 RA "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N and O
 RT isolates provides an alternative region for the determination."
 RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RI EMBL: Y09775; CAAT0914.1; -
 DR INTERPRO: IPR000328; -
 DR PFAM: PF00517; GP41; 1.
 KW Envelope protein.
 FT NON_TER 1 1
 FT NON_TER 131 131
 SO SEQUENCE 131 AA: 15736 MW: 1053F85345F8B98 CRC64:

Fri Mar 23 07:47:50 2001

us-09-147-362-15.rpt

Best Local Similarity 81.5%; Pred. No. 1e-10;
Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSMCKGRVCTYSV 28
|||||: ||||| ||||| ||||| |||||
DB 65 ALETLNQRLNSMCKGRVCTYSV 91

RESULT 15

ID 09IEB9 PRELIMINARY; PCT: 532 AA.
AC 09IEB9; 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE ENV POLYPEPTIDE (FRAGMENT).
OS HIV POLYPEPTIDE (FRAGMENT).
OR Human immunodeficiency virus type 1.
VS Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
[1]
NM SEQUENCE FROM N.A.
RP STRAIN: HIV-1
RC Roberton D., Diamond P., Sousquiere S., Mauciere P.,
RA Deplenne C., Brun-Vezinet F., Dormont D.:
RT "HIV-1 group O phylogenetic analysis of C2-Vif region",
DR EMBL: AJ133058; CAB96219.1; -
FT NON_TER 532
FT 532
SQ SEQUENCE 532 AA: 55688 MW: 3761D740D858A760 CRG64:

Query Match 81.2%; Score 121; DB 12; Length 532;
Best Local Similarity 81.3%; Pred. No. 1e-10;
Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSMCKGRVCTYSV 28
|||||: ||||| ||||| ||||| |||||
DB 354 ALETLNQRLNSMCKGRVCTYSV 380

Search completed: March 22, 2001, 10:00:47
Job time: 526 sec

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GenCore version 4.5
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OM protein - protein search, using SW model

Run on: March 22, 2001, 09:57:52 ; Search time 29.4 Seconds
(without alignments)
30.756 Million cell updates/sec

Title:	US-09-147-362-15
Perfect score:	149
Sequence:	1 RAETLLNQORLLNSWCGKGRLCVYTSV 28

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      88757 seqs, 32294092 residues
              total number of hits satisfying chosen parameters: 88757
```

```

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

```

```

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

Database : SWISSProt_39:4

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result					Query		ID	Description
No.	Score	Match	Length	DB				
1	85	57	0	854	1	ENV_HV2KZ	P17261	chlamydiae
2	85	56	4	857	1	ENV_HV2KZ	O7416	human
3	85	55	0	843	1	ENV_HV12	P19550	human
4	82	55	0	847	1	ENV_HV1S1	P19550	human
5	82	55	0	847	1	ENV_HV1M2	P05880	human
6	82	55	0	851	1	ENV_HV1M2	P04582	human
7	82	55	0	852	1	ENV_HV1M1	P12488	human
8	82	55	0	852	1	ENV_HV1M3	P19549	human
9	82	55	0	853	1	ENV_HV1S1	P19551	human
10	82	55	0	855	1	ENV_HV1M2	P12457	human
11	82	55	0	855	1	ENV_HV1A2	P03268	human
12	82	55	0	855	1	ENV_HV1A2	P03268	human
13	82	55	0	855	1	ENV_HV1A2	P04580	human
14	82	55	0	855	1	ENV_HV1A2	P03375	human
15	82	55	0	856	1	ENV_HV1B1	P04578	human
16	82	55	0	856	1	ENV_HV1M1	O70628	human
17	82	55	0	856	1	ENV_HV1M1	P05887	human
18	82	55	0	856	1	ENV_HV1PV	P03376	human
19	82	55	0	856	1	ENV_HV1M1	P05878	human
20	82	55	0	856	1	ENV_HV1M1	P12488	human
21	82	55	0	856	1	ENV_HV1A1	P03377	human
22	82	55	0	856	1	ENV_HV2M2	P04579	human
23	82	55	0	851	1	ENV_HV1B1	P04579	human
24	82	55	0	855	1	ENV_HV1B1	P12488	human
25	82	55	0	857	1	ENV_HV1C4	P05878	human
26	80	53	7	856	1	ENV_HV1B1	P20871	human
27	80	53	7	856	1	ENV_HV1B1	P04624	human
28	79	53	0	711	1	ENV_HV2S2	P12325	human
29	79	53	0	851	1	ENV_HV2D1	P18040	human
30	79	53	0	851	1	ENV_HV2S1	O02873	human
31	79	53	0	851	1	ENV_HV1A1	P05881	human
32	79	53	0	856	1	ENV_HV1A1	P04577	human
33	79	53	0	858	1	ENV_HV2B0		human

34	79	859	1	ENV_HVZCA	P24015 human	human
35	79	859	1	ENV_HVZD2	P15831 human	human
36	79	859	1	ENV_HVST	P20872 human	human
37	79	860	1	ENV_HVST	P18094 human	human
38	78	860	1	ENV_HVST	P20482 simian	human
39	79	865	1	ENV_STVAT	P15053 simian	human
40	79	885	1	ENV_STVSA	P18759 human	human
41	78	889	1	ENV_STVSP	P18449 human	human
42	77	846	1	ENV_HVSD	P04583 human	human
43	77	863	1	ENV_HVMA	P05882 human	human
44	76	863	1	ENV_HVMA	P08810 simian	human
45	76	380	1	ENV_STVW2		

ALIGNMENTS

[illegible]

Query Match
 Seq. Local Similarity 57.0%; Score 85; DB 1; Length 854;
 Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 2 ALETLMDORILNSMCKGRLWCTYSV 28
 DB 572 AVERILMDORILNSMCKGRLWCTTV 598

RESULT 2
 ENV_HVZR STANDARD; PRT; 857 AA.
 AC 074126;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ENV_HVZR
 DE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
 GLYCOPROTEIN (GP120), TRANSMEMBRANE GLYCOPROTEIN (GP41)].
 OS Human immunodeficiency virus type 2 (Isolate KR) (HIV-2).
 NC Viruses; Retroviral; Lentivirus.
 RN 11
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 modified non-profit institutions as long as its content is not removed, usage by
 or send an email to license@ebi.ac.uk or <http://www.isb-sib.ch/announce/>

FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 854 AA; 59803 MW; 262349A06F2D9B3 CRC64; .
 SIGNAL.
 FT CHAIN 1 19 POTENTIAL.
 FT CHAIN 20 503 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CARBOHYD 36 857 TRANSMEMBRANE GLYCOPROTEIN.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 152 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match
 Seq. Local Similarity 56.4%; Score 84; DB 1; Length 857;
 Matches 16; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
 2 ALETLMDORILNSMCKGRLWCTYSV 28
 DB 573 AVERILMDORILNSMCKGRLWCTTV 599

RESULT 3
 ENV_HVY2 STANDARD; PRT; 843 AA.
 AC P35961;
 DT 01-JUN-1994 (Rel. 28, Created)
 DT 15-JUL-1999 (Rel. 29, Last annotation update)
 DE ENV_HVY2
 DE ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
 GLYCOPROTEIN (GP120), TRANSMEMBRANE GLYCOPROTEIN (GP41)].
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
 NC Viruses; Retroviral; Lentivirus.
 RN 11
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FT CARBOHYD 264 264 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 857 AA; 98689 MW; P8B1C675B85740DF CRC64; .
 SIGNAL.
 FT CHAIN 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 30 489 TRANSMEMBRANE GLYCOPROTEIN.
 FT TRANSMEM 738 738 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT TRANSMEM 773 773 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 118 201 BY SIMILARITY.
 FT DISULFID 125 192 BY SIMILARITY.
 FT DISULFID 130 155 BY SIMILARITY.
 FT DISULFID 214 243 BY SIMILARITY.
 FT DISULFID 224 235 BY SIMILARITY.

Qy 2 ALETLANDORLINSCKCKGRVLQVTSV 28
 1:1 1:1 1:1 1:1 1:1 1:1
 Db 569 AVERVLRDQDLGIMCGSKGLCTIVV 595
 RESULT 4
 ENLPIVSI
 AD ENLPIVSI STANDARD: PRT: 847 AA.
 PI95501
 01-FEB-1991 (Rel. 17, Created)
 01-FEB-1991 (Rel. 17, Last sequence update)
 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE
 G120): TRANSMEMBRANE GP162 ISOLEIN (GP441).
 GN ENV.
 OS Human immunodeficiency virus type 1 (SP162 isolate) (HIV-1).
 OS Viruses: Retroid viruses; Retroviridae; Lentiviruses.
 RN [1]
 RN SOURCE REFERENCE FROM N.A.
 RA MEDLINE=60347835; PubMed=2384920;
 RA Cheng-Hayer C., Quirica M., Tung J.W., Dina D., Levy J.:
 "Viral determinants of human immunodeficiency virus type 1 T-cell or
 macrophage tropism, cytopathogenicity, and CCR5 antigen modulation." J
 Virol. 64:4390-4396(1990).
 RL CC
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 CC or send an email to license@sb.sib.ch).
 DR EMBL: M65024; AAAA5072.1; .
 DR HIV: M88428; ENVSF612.

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Query Match      55.0%   Score 82:  DB 1:  Length 847:
Best Local Similarity 51.9%:   Pred. No. 9,9e-05:
Matches 14:  Conservative  5:  Mismatches  8:  Indels  0:  Gaps  0:

QY      2 ALETLINQORLLNSGCKGLRVCYSV 28
      1:1 1:1 1:1 1:1 1:1 1:1 1:1
Db      573 AVERILKDDQDLGIGSGKSLCTIAV 599

RESULT  5
ID  ENV_HV1w2      STANDARD:  PRT:  847 AA.
AC  P05880:
DF  01-NOV-1988 (Rel. 09, Created)
DF  01-NOV-1988 (Rel. 09, Last sequence update)
DE  ENVELOPE POLYPEPTIDE IN GLIO PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE  GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
OS  ENV.
CN  Human immunodeficiency virus type 1 (HIV-1) isolate (HIV-1).
CC  Viruses; Retroid Viruses; Retroviridae; Lentivirus.
NM  SEQUENCE FROM N.A.
RX  MEDLINE=86235450; PubMed=3012778;
RA  Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
   *Salathuddin S.Z., Wong-Staal F., Gallo R.C., Parks W.C., P.
   *Genetic variation in HIV-1/IIIVa over time in patients with AIDS or

```


Query Match 55.0%; Score 82; DB 1; Length 851;
Best Local Similarity 51.9%; Pred. No. 9.9e-05;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

2 ALETLNMOGLNMGCGRLGCTVSV 28
577 AVERLMDQDLGIMGCGRLGCTTAV 603

ENV_HV18N STANDARD; PRT: 852 AA.

AC P12488; (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)]
GN ENV.
OS Human immunodeficiency virus type 1 (JR9 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN MEDLINE-99085613; Pubmed-2789516;
RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Lucif P., Dandekar S.;
RT "Biological and molecular characterization of human immunodeficiency virus (HIV-188) from the brain of a patient with progressive dementia." 16:79-89 (1989).
RT VIROLOGY 16:79-89 (1989).
CC -1- HAVESSED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
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CC EMBL: M21098; AAA44221.1;
DR PIR: A11667; VCLBR.
DR HIV: M21098; ENV589A.
DR INTERPRO: IPR00327;
DR DRAM: P000516; GP120. 1.
DR PFM: P000517; GP41. 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
KW SIGNAL. 30
FT CHAIN 31 30 EXTENSOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 32 30 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 218 155 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 236 BY SIMILARITY.
FT DISULFID 236 239 BY SIMILARITY.
FT DISULFID 383 412 BY SIMILARITY.

ENV_HV18N STANDARD; PRT: 852 AA.

AC P12488; (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)]
GN ENV.
OS Human immunodeficiency virus type 1 (JR9 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN MEDLINE-99085613; Pubmed-2789516;
RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Lucif P., Dandekar S.;
RT "Biological and molecular characterization of human immunodeficiency virus (HIV-188) from the brain of a patient with progressive dementia." 16:79-89 (1989).
RT VIROLOGY 16:79-89 (1989).
CC -1- HAVESSED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
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CC EMBL: M21098; AAA44221.1;
DR PIR: A11667; VCLBR.
DR HIV: M21098; ENV589A.
DR INTERPRO: IPR00327;
DR DRAM: P000516; GP120. 1.
DR PFM: P000517; GP41. 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
KW SIGNAL. 30
FT CHAIN 31 30 EXTENSOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 32 30 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 218 155 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 236 BY SIMILARITY.
FT DISULFID 236 239 BY SIMILARITY.
FT DISULFID 383 412 BY SIMILARITY.

Query Match 55.0%; Score 82; DB 1; Length 852;
Best Local Similarity 51.9%; Pred. No. 9.9e-05;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

2 ALETLNMOGLNMGCGRLGCTVSV 28
578 AVERLMDQDLGIMGCGRLGCTTAV 604

ENV_HV18N STANDARD; PRT: 852 AA.

AC P12488; (Rel. 12, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)]
GN ENV.
OS Human immunodeficiency virus type 1 (JR9 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN MEDLINE-90317906; Pubmed-2370688;
RA Yori-Higashida D., Meng J., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range, human immunodeficiency virus type 1 cellular host range, and cytopathicity are linked to the envelope region of the viral genome." 6:4016-4020 (1990).
CC -1- HAVESSED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
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CC EMBL: M38427; AAA45067.1;
DR HIV: M38427; ENV589A.
DR INTERPRO: IPR00327;

[illegible]

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RA Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier G.,
RA Waslak A.;
RT "Cloning and characterization of human immunodeficiency virus type 1
RT variants diminished in the ability to induce syncytium-independent
RT cytolysis."
RL J Virol 64:3792-3803(1990).
CC -----
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DR EMBL; M39343; AAA44850.1;
DR HIV; M39343; ENVSPMA;
DR INTERPRO; IPR000328;
DR INTERPRO; IPR000777;
DR PDB; PF00516; GP120_1;
DR Pfam; PF0517; GP1; 1;
KW Signal. Coat protein. Polyprotein. Glycoprotein. Transmembrane;
PT SIGNAL 1 30
PT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
PT GRAIN 510 853 TRANSMEMBRANE GLYCOPROTEIN.
PT DISULFID 514 74 BY SIMILARITY.
PT DISULFID 119 203 BY SIMILARITY.
PT DISULFID 131 154 BY SIMILARITY.
PT DISULFID 216 237 BY SIMILARITY.
PT DISULFID 226 245 BY SIMILARITY.
PT DISULFID 294 329 BY SIMILARITY.
PT DISULFID 376 443 BY SIMILARITY.
PT DISULFID 383 416 BY SIMILARITY.
PT DISULFID 438 468 BY SIMILARITY.
PT GRAIN 469 1088 EXTERIOR MEMBRANE GLYCOPROTEIN.
PT CHAIN 1089 1461 TRANSMEMBRANE GLYCOPROTEIN.
PT GRAIN 1462 1561 TRANSMEMBRANE GLYCOPROTEIN.
PT CARBOHYD 1562 160 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAc ...) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAc ...) (POTENTIAL).
SO SEQUENCE 853 AA; 96912 MW; 3377B93B6F2ABA CRC64;
Query Match Score 82; DB 1; Length 853;
Best Local Similarity 51.9%; Percent No. 9.3e-05;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

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Query Match 73.8%; Score 110; DB 2; Length 877;
 Best Local Similarity 70.4%; Pred. No. 2e-08;
 Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Oy 2 ALETLNMOQLINMGCKRGKVCYTSV 28
 Db 597 ALETLNMOQLINMGCKRGKVCYTSV 623

RESULT 3
 SS2930
 G41 ENV protein - human immunodeficiency virus type 1 (fragment)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 20-Feb-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
 C:Accession: S52930
 R:Steuiler, H.; Storch-Hagenlocher, B.; Philibert, F.; Chararet, S.; Tabary, T.; Montagnier, L.; de
 submitted to the EMBL Data Library, January 1995
 A:Description: A novel HIV-1 strain illustrates the diversity of the O group.
 Reference number: S52929
 Accession: S52930
 A:Status: preliminary
 A:Residues: 1-104 <STP>
 A:Cross-references: EMBL:X84328; NID:9695526; PIDN:CAA5906.1; PID:9695527
 C:Superfamily: type E retrovirus env polyprotein

Query Match 73.2%; Score 109; DB 2; Length 104;
 Best Local Similarity 66.7%; Pred. No. 3.5e-09;
 Matches 18; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 Oy 2 ALETLNMOQLINMGCKRGKVCYTSV 28
 Db 35 ALETLNMOQLINMGCKRGKVCYTSV 61

RESULT 4
 SS2190
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S2190
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 submitted to the EMBL Data Library, July 1991
 A:Reference number: S2190
 A:Status: preliminary
 A:Residues: 1-357 <STP>
 A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
 C:Superfamily: type E retrovirus env polyprotein

Query Match 57.0%; Score 85; DB 2; Length 357;
 Best Local Similarity 55.6%; Pred. No. 4.5e-05;
 Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 Oy 2 ALETLNMOQLINMGCKRGKVCYTSV 28
 Db 83 ALETLNMOQLINMGCKRGKVCYTSV 109

RESULT 5
 S70423
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 20) (fragment)
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Variety: patient 20
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
 C:Accession: S70423
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8:53-58, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb

A:Reference number: S70417; NID:92144209
 A:Accession: S70423
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <STP>
 A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
 C:Superfamily: type E retrovirus env polyprotein

Query Match 57.0%; Score 85; DB 2; Length 357;
 Best Local Similarity 55.6%; Pred. No. 4.5e-05;
 Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 Oy 2 ALETLNMOQLINMGCKRGKVCYTSV 28
 Db 83 ALETLNMOQLINMGCKRGKVCYTSV 109

RESULT 6
 SS2002
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S22002
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 submitted to the EMBL Data Library, July 1991
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as de
 A:Reference number: S2190
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-358 <STP>
 A:Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187
 C:Superfamily: type E retrovirus env polyprotein

Query Match 57.0%; Score 85; DB 2; Length 358;
 Best Local Similarity 55.6%; Pred. No. 4.3e-05;
 Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 Oy 2 ALETLNMOQLINMGCKRGKVCYTSV 28
 Db 84 ALETLNMOQLINMGCKRGKVCYTSV 110

RESULT 7
 S70418
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 31) (fragm
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Variety: patient 31
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
 C:Accession: S70418
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8:53-58, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
 A:Reference number: S70417; NID:92144209
 A:Accession: S70418
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-358 <STP>
 A:Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187
 C:Superfamily: type E retrovirus env polyprotein

Query Match 57.0%; Score 85; DB 2; Length 358;
 Best Local Similarity 55.6%; Pred. No. 4.5e-05;
 Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 Oy 2 ALETLNMOQLINMGCKRGKVCYTSV 28
 Db 84 ALETLNMOQLINMGCKRGKVCYTSV 110

```
DB      572  ATATGTAAGDQDGLSLMGCGAACCCTTIV 598
RESULT 10
AA5713
env transmembrane protein gp43 - human immunodeficiency virus type 2
C:Accession: AA5713
C:Date: 04-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
R:Hannett, S.W.; Quiroga, M.; Wernert, A.; Dina, D.; Levy, J.A.
J. Virol. 67, 1006-1014, 1993
A:Title: Distinguishing features of an infectious molecular clone of the highly
A:Accession: AA5713
A:Keywords: HIV; AIDS
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-855 <BAF>
A:Experimental source: UCI
A:Note: sequence extracted from NCBI backbone (NCBIF:122352)
C:Superfamily: type B retrovirus env polypeptide
Query Match          57.0%; Score 85; DB 2; Length 855;
Best Local Similarity 59.3%; Pval. No. 0.00011;
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
```

```

Db      584  ALEKYLIDQALLNSMCAFRQVCHTTV 610
      11::11 11111111 11111111
RESULT 11
envelope protein gp120/gp41 - human immunodeficiency virus type 1
S22000
C1:Species: human immunodeficiency virus type 1, HIV-1

```

C:Accession: S22000
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-358 <Str>
A:Cross-references: EMBL:X61351
C:Superfamily: type E retrovirus env polypeptide

[illegible]

A:Title: Distinct populations of human immunodeficiency virus type A in blood and
A:Reference number: S70417; M01D:92144209
A:Accession: S70417
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-358 <STE>
A:Cross-references: EMBL:x61351; NID:g60184; PIRN:CAA43614.1; PTD:g60185
C:Superfamily: type E retrovirus env polypotein

Fri Mar 23 07:47:48 2001

us-09-147-362-15.rpt

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Query match	Pred. No.
Best local Similarity	1.1e-12;
85.28;	

Query Match	85.28;	Score 127;	DB 3;	Length 33;
Best Local Similarity	85.28;	Pred. No. 1.1e-12;		

Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALETLNNOGLNLSMCKGRIVCTSV 28
 |||||:|||||
 DB 4 ALETLNNOGLNLSMCKGRIVCTSV 30

RESULT 3
 US-08-894-699-39

; Sequence 39, Application US/08894699

; Patent No. 6030769

; GENERAL INFORMATION:

; APPLICANT: SIMON, FRANCOIS

; APPLICANT: SARACOSTI, SENTOB

; APPLICANT: LOUSSEY-AJAKA, IBITISSAM

; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" floppy disk

; OPERATING SYSTEM: IBM PC COMPATIBLE

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION NUMBER: US/08/894,699

; FILING DATE: 01-DEC-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR96/00294

; FILING DATE: 26-FEB-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 95/02236

; FILING DATE: 27-FEB-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 39:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 40 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Peptide

; US-08-894-699-39

Query Match 85.2%; Score 127; DB 3; Length 40;

Best Local Similarity 85.2%; Pred. No. 1,4e-12;

Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALETLNNOGLNLSMCKGRIVCTSV 28

|||||:|||||
 DB 9 ALETLNNOGLNLSMCKGRIVCTSV 35

RESULT 4

US-08-894-699-60

; Sequence 68, Application US/08894699

; Patent No. 6030769

; GENERAL INFORMATION:

; APPLICANT: SIMON, FRANCOIS

; APPLICANT: SARACOSTI, SENTOB

; APPLICANT: LOUSSEY-AJAKA, IBITISSAM

; APPLICANT: LI, THOI-DUONG

; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC COMPATIBLE

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/894,699

; FILING DATE: 01-DEC-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR96/00294

; FILING DATE: 26-FEB-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 95/02236

; FILING DATE: 27-FEB-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 68:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 40 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Peptide

; US-08-894-699-68

Query Match 85.2%; Score 127; DB 3; Length 40;

Best Local Similarity 85.2%; Pred. No. 1,4e-12;

Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALETLNNOGLNLSMCKGRIVCTSV 28

|||||:|||||
 DB 9 ALETLNNOGLNLSMCKGRIVCTSV 35

RESULT 5

US-09-433-4280-30

; Sequence 30, Application US/094334280

; Patent No. 6149910

; GENERAL INFORMATION:

; APPLICANT: De Leys, Robert J.

; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

; FILING DATE: US-20-09-11-04

; CURRENT APPLICATION NUMBER: US/09/433,4280

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: Patentin Ver. 2.0

SPD ID NO 30
 LENGTH: 33
 TYPE: PRF
 ORGANISM: Human immunodeficiency virus type 1
 US-09-433-428D-30

Query Match 83.9% Score 125; DB 3; Length 33;
 Best Local Similarity 81.5% Pred. No. 2,2e-12;

Matches 22: Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETLNQGRLNSMCKGRVCTSV 28
 ||||| : ||||| ||||| |||||
 DB 4 ALETLNQGRLNSMCKGRVCTSV 30

RESULT 6
 US-08-894-699-36
 Sequence 36, Application US/08894699
 Patent No. 6030769

GENERAL INFORMATION:
 APPLICANT: SIMON, FRANCOIS
 APPLICANT: SARAGOSTI, JACQUES
 APPLICANT: LEBLANC, JACQUES
 APPLICANT: LY, THOI-DUONG
 APPLICANT: CHAIX-BAUDIER, MARIE-LOUISE
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/08/894,699
 FILING DATE: 01-DEC-1997
 CLASSIFICATION: DATA
 PRIOR APPLICATION: PCT/FR96/00294
 FILING DATE: 26-FEB-1996
 APPLICATION DATA:
 APPLICATION NUMBER: FR 95/02236
 FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 34,614
 TELEPHONE NUMBER: 0154-0020-OPCT
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-894-699-36

Query Match 83.9% Score 125; DB 3; Length 40;
 Best Local Similarity 81.5% Pred. No. 2,7e-12;
 Matches 22: Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETLNQGRLNSMCKGRVCTSV 28
 ||||| : ||||| ||||| |||||
 DB 9 ALETLNQGRLNSMCKGRVCTSV 35

RESULT 7
 US-09-433-428D-4
 Sequence 4, Application US/09433428D
 Patent No. 6145910

GENERAL INFORMATION:
 APPLICANT: De Leys, Robert J.

FILE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O.

CURRENT FILING DATE: 1999-11-04
 NUMBER OF SEQ ID NOS: 70
 SPID ID NO 4
 LENGTH: 33
 TYPE: PRF

US-09-433-428D-4
 ORGANISM: Human immunodeficiency virus type 1

Query Match 81.2% Score 121; DB 3; Length 33;
 Best Local Similarity 81.5% Pred. No. 8,7e-12;
 Matches 22: Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQGRLNSMCKGRVCTSV 28
 ||||| : ||||| ||||| |||||
 DB 4 ALETLNQGRLNSMCKGRVCTSV 30

RESULT 8
 US-09-433-428D-7
 Sequence 7, Application US/09433428D
 Patent No. 6145910

GENERAL INFORMATION:
 APPLICANT: De Leys, Robert J.

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
 CURRENT FILING DATE: 1999-11-04
 NUMBER OF SEQ ID NOS: 70
 SOFTWARE: Patent Ver. 2.0
 SPID ID NO 7
 LENGTH: 33
 TYPE: PRF

US-09-433-428D-7
 ORGANISM: Human immunodeficiency virus type 1

Query Match 81.2% Score 121; DB 3; Length 33;
 Best Local Similarity 81.5% Pred. No. 8,7e-12;
 Matches 22: Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQGRLNSMCKGRVCTSV 28
 ||||| : ||||| ||||| |||||
 DB 4 ALETLNQGRLNSMCKGRVCTSV 30

RESULT 9
 US-09-433-428D-15
 Sequence 15, Application US/09433428D
 Patent No. 6145910

GENERAL INFORMATION:
 APPLICANT: De Leys, Robert J.

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
 CURRENT FILING DATE: 1999-11-04
 NUMBER OF SEQ ID NOS: 70
 SOFTWARE: Patent Ver. 2.0
 SPID ID NO 15
 LENGTH: 33
 TYPE: PRF


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RESULT 12
US-09-433-428D-5
: Sequence 5, Application US/09433428D
: Patent No. 6149910
: GENERAL INFORMATION:
: APPLICANT: De Leys, Robert J.
: TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
: FILE REFERENCE: CDS-207
: CURRENT APPLICATION NUMBER: US/09/433,428D
: CURRENT FILING DATE: 1999-11-04
: NUMBER OF SEQ. ID NOS: 70
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 33
: TYPE: PRN
: ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-5
Query Match
: 80.5%; Score 120; DB 3; Length 33;
: Best Local Similarity 77.8%; Pred. No. 1,2e-11;
: Matches 21; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 2 ALETLNMOURLNSWCKGRKLCYTSV 28
DB 4 ALETLNMOURLNSWCKGRKLCYTSV 30
RESULT 13
US-09-433-428D-8
: Sequence 6, Application US/09433428D
: Patent No. 6149910
: GENERAL INFORMATION:
: APPLICANT: De Leys, Robert J.
: TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
: FILE REFERENCE: CDS-207
: CURRENT APPLICATION NUMBER: US/09/433,428D
: CURRENT FILING DATE: 1999-11-04
: NUMBER OF SEQ. ID NOS: 70
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 8
: LENGTH: 33
: TYPE: PRN
: ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-8
Query Match
: 80.5%; Score 120; DB 3; Length 33;
: Best Local Similarity 77.8%; Pred. No. 1,2e-11;
: Matches 21; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 2 ALETLNMOURLNSWCKGRKLCYTSV 28
DB 4 ALETLNMOURLNSWCKGRKLCYTSV 30

```

```

: TYPE: PRN
: ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-16
Query Match
: 80.5%; Score 120; DB 3; Length 33;
: Best Local Similarity 77.8%; Pred. No. 1,2e-11;
: Matches 21; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 2 ALETLNMOURLNSWCKGRKLCYTSV 28
DB 4 ALETLNMOURLNSWCKGRKLCYTSV 30
RESULT 15
US-08-894-699-67
: Sequence 67, Application US/08894699
: Patent No. 6030769
: GENERAL INFORMATION:
: APPLICANT: SARACOSI, SENIOR
: APPLICANT: LOUSSET-AJAKA, IBITISSAM
: APPLICANT: LY, THOI-DUONG
: APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
: TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
: NUMBER OF SEQUENCES: 91
: NUMBER OF SEQ. IDS: 85
: ADDRESSER: GILON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
: ADDRESSER: P.C.
: STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
: CITY: ARLINGTON
: STATE: VA
: COUNTRY: USA
: DATE OF INVENTION: 2000
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/894,699
: FILING DATE: 01 DEC 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/FR96/00294
: FILING DATE: 26-FEB-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 95/02236
: FILING DATE: 27-FEB-1995
: ATTORNEY/AGENT INFORMATION:
: REGISTRATION NUMBER: 24,614
: REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-413-3000
: TELEFAX: 703-413-2220
: INFORMATION FOR SEQ ID NO: 67:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 41
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-894-699-67
Query Match
: 80.5%; Score 120; DB 3; Length 41;
: Best Local Similarity 77.8%; Pred. No. 1,6e-11;
: Matches 21; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 2 ALETLNMOURLNSWCKGRKLCYTSV 28

```

Fri Mar 23 07:47:46 2001

us-09-147-362-15.rail

Page 6

||||: ||||| |||||:|||||
db 9 ALSTLIONOOLINLMGCKRCLCYTSV 35

Search completed: March 22, 2001, 09:52:45
Job time: 123 sec

Genome version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 09:51:54 : Search time 65.29 Seconds
(without alignments)
14.664 Million cell updates/sec

Title: US-09-147-362-15

Perfect score: 149

Sequence: 1 KALETLINQORHLNMGKGRILVCYSV 28

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1. /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
2. /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
3. /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
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6. /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*
7. /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT:*
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12. /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*
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18. /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*
19. /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*
20. /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
21. /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	149	100.0	28	19	W80473
2	127	85.2	40	17	W07351
3	126	83.6	40	17	W07352
4	125	83.9	40	17	W07353
5	122	81.9	22	19	W80472
6	122	81.9	42	17	W07354
7	121	81.2	41	17	W07355
8	121	81.2	42	17	W07356
9	121	81.2	116	20	Y05555
10	121	81.2	117	20	Y05556
11	121	81.2	715	20	Y05557
12	120	80.5	32	19	W80470

13	120	80.5	41	17	W07351	Partial sequence o
14	120	80.5	113	20	Y05559	HIV-1 group O 1801
15	120	80.5	115	20	Y05557	HIV-1 group O 1801
16	120	80.5	200	21	Y77373	HIV-1 group O env
17	120	80.5	215	20	Y09499	HIV-1 group O env
18	120	80.5	215	20	Y09499	Recombinant pCO-8P
19	120	80.5	215	21	Y77374	Recombinant pCO-8P
20	120	80.5	243	21	Y09499	HIV-1 group O env
21	120	80.5	245	21	Y77369	HIV-1 group O env
22	120	80.5	281	20	Y09507	Recombinant pCO-9P
23	120	80.5	373	20	Y09495	HIV-1 group O pCO-
24	120	80.5	373	20	Y09495	HIV-1 group O env
25	120	80.5	460	20	Y09500	Recombinant pCO-11
26	120	80.5	460	20	Y09500	Recombinant pCO-8C
27	120	80.5	460	21	Y77375	HIV-1 group O env
28	120	80.5	474	21	Y77375	HIV-1 group O env
29	120	80.5	480	21	Y09499	HIV-1 group O env
30	120	80.5	480	20	Y09494	HIV-1 group M and
31	120	80.5	490	20	Y06978	Recombinant pCO-9C
32	120	80.5	490	20	Y06978	HIV-1 group O poly
33	120	80.5	526	20	Y09505	HIV-1 group O env
34	120	80.5	526	20	Y09505	Recombinant pCO-11
35	120	80.5	618	20	Y06980	Recombinant pCO-11
36	120	80.5	618	21	Y77372	HIV-1 group M and
37	120	80.5	618	21	Y77372	HIV-1 group M and
38	120	80.5	736	20	Y09502	HIV-1 group M and
39	120	80.5	736	20	Y09502	HIV-1 group M and
40	120	80.5	873	20	Y09561	HIV-1 group O env
41	120	80.5	873	20	Y09561	Amino acid sequenc
42	120	80.5	873	21	Y77376	HIV-1 group O 1801
43	119	79.9	110	20	Y05552	HIV-1 group O 1801
44	119	79.9	110	20	Y05553	HIV-1 group O 1801
45	119	79.9	113	20	Y05551	HIV-1 group O 1801

ALIGNMENTS

RESULT 1	W80473	standard; peptide: 28 AA.
ID	W80473	
AC	W80473	
DT	28-JAN-1999	(first entry)
DE	Peptide derived from a conserved sequence of group O human HIV.	
KW	Group O human immune deficiency virus; HIV; detection: Infection.	
OS	Synthetic.	
XX	Immune deficiency virus.	
XX	W09845323-AL.	
PD	15-OCT-1998.	
XX		
PF	06-APR-1998; 98MO-FR00651.	
PR	24-FEB-1998; 98FR-0002312.	
XX	09-APR-1997; 97FR-0004356.	
XX	(SNFI) PASTEUR SANOPI DIAGNOSTICS SA.	
XX	Cheneboux DMB, Delagrange JFH, Gabelle SXH, Rieunier FY;	
XX	WPI: 1996-583190/49.	
XX	New synthetic peptide(s) - useful for e.g. detecting infection by	
XX	human immune deficiency virus of group O	
XX	Claim 6: Page 44: 55pp: French.	

CC M80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent the amino acid sequences
 CC connected around short highly conserved sequences present in peptides
 CC of group O human immunodeficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immunodeficiency virus (HIV).
 SQ Sequence 28 AA:

Query Match 100.0%; Score 149; DB 19; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2, Gc-14;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLNMOORLNSMGCKGLVCTSY 28
 DB 1 alettlngqlnswgckgrlvcysv 28

RESULT 2

W07346 standard; peptide: 40 AA.

W07346:

03-JUN-1997 (first entry)

Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).

Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;
 C23-env; gp41; 999; retrovirus; strain; gp120; hypervariable loop;
 primer; hybridisation; amplification; PCR; polymerase chain reaction;
 immunogen; antibody.

Human immunodeficiency virus type 1.

W09627013-A1.

06-SEP-1996.

26-FEB-1996; 96MO-FR00294.

27-FEB-1995; 95FR-0002236.

(ASST-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;

WPI: 1996-412779/41.
 N-PSDB: T44922.

New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 PT antibodies - useful for diagnosis, screening and typing, or as
 PT immunogens

Claim 12; Page 34; 71pp: French.

Human immunodeficiency virus type 1 (HIV-1) strains are currently divided
 CC into 2 major groups based on the nucleotide sequences of the envelope gene
 CC (env); group M containing sub-groups A-G, and group O containing the
 CC strains ANR70 and WPS180. The invention relates to the discovery of
 CC several new strains of HIV-1 which can be placed in group O, based on the
 CC partial sequences of the C23-env, gp41 and gag genes (see T44907-39 and
 CC W07329-64). The novel strains have been deposited as retroviruses CCM
 CC T-1544 (BCP02 (ESS)), 1543 (BCP01 (FAN)), 1546 (BCP07 (MAN)) and
 CC (MKO) and 1545 (BCP03 (POC)). The sequence presented here is from the
 CC strain BCF07 (MAN) and corresponds to a fragment of the gp41 protein
 CC encoded by the env gene. The nucleic acids can be used to detect gp. O
 CC strains by hybridisation or (as primers) by gene amplification, or
 CC also for screening and typing of such strains. Peptides encoded by the
 CC nucleic acids can be used as immunogens to raise Ab for detecting gp. O
 CC HIV-1.

XX Sequence 40 AA:
 SQ Query Match 95.2%; Score 127; DB 17; Length 40;
 Best Local Similarity 95.2%; Pred. No. 4, 2c-11;
 Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALETLNMOORLNSMGCKGLVCTSY 28
 DB 9 alettlngqlnswgckgrlvcysv 35

RESULT 3

W07352 standard; peptide: 40 AA.

W07352:

03-JUN-1997 (first entry)

Partial sequence of gp41 from HIV-1 gp. O strain BCF13.

Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;
 C23-env; gp41; 999; retrovirus; strain; gp120; hypervariable loop;
 primer; hybridisation; amplification; PCR; polymerase chain reaction;
 immunogen; antibody.

Human immunodeficiency virus type 1.

W09627013-A1.

06-SEP-1996.

26-FEB-1996; 96MO-FR00294.

27-FEB-1995; 95FR-0002236.

(ASST-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;

WPI: 1996-412779/41.

New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 PT antibodies - useful for diagnosis, screening and typing, or as
 PT immunogens

Claim 12; Page 46; 71pp: French.

Human immunodeficiency virus type 1 (HIV-1) strains are currently divided
 CC into 2 major groups based on the nucleotide sequences of the envelope gene
 CC (env); group M containing sub-groups A-G, and group O containing the
 CC strains ANR70 and WPS180. The invention relates to the discovery of
 CC several new strains of HIV-1 which can be placed in group O, based on the
 CC partial sequences of the C23-env, gp41 and gag genes (see T44907-39 and
 CC W07329-64). The novel strains have been deposited as retroviruses CCM
 CC T-1544 (BCP02 (ESS)), 1543 (BCP01 (FAN)), 1546 (BCP07 (MAN)) and
 CC (MKO) and 1545 (BCP03 (POC)). The sequence presented here is from the
 CC strain BCF13 and corresponds to a fragment of the gp41 protein
 CC encoded by the env gene. The nucleic acids can be used to detect gp. O
 CC strains by hybridisation or (as primers) by gene amplification, or
 CC also for screening and typing of such strains. Peptides encoded by the
 CC nucleic acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.

Sequence 40 AA:

Query Match 85.2%; Score 127; DB 17; Length 40;
 Best Local Similarity 85.2%; Pred. No. 4, 2c-11;
 Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;


```

OY 2 ALETTILNMOORLLNSMCKGKGLVCTYSV 28
DB 9 alettlmqqlinswgcgrlvcysv 35

RESULT 4
ID W80469 standard; peptide: 32 AA.
W80469:
28-JAN-1999 (first entry)
Peptide derived from a conserved sequence of group O human HIV.
DE Group O human immune deficiency virus; HIV; detection; infection.
XX Synthetic.
XX Immune deficiency virus.
XX W09845323-AL.
XX PD 15-OCT-1998.
XX PF 06-APR-1998; 98MO-FR00691.
XX XX 24-FEB-1998; 98FR-0002212.
XX PR 09-APR-1997; 97FR-0004356.
XX XX (SNF) PASTEUR SANCOTI DIAGNOSTICS SA.
XX PI Cheneboux DMB, Delagrange JFH, Gabelle SX, Rieunier FY;
XX WPI: 1996-583190/49.
XX DR New synthetic peptide(s) - useful for, e.g. detecting infection by
XX PT human immune deficiency virus of group O
XX PS Claim 6; Page 44; 55pp; French.
XX CC W80459-74 represent synthetic peptides (either linear or cyclised by
XX CC Cys-Cys disulphide bridges). The peptides represent variable sequences
XX CC of group O human immune deficiency virus (HIV). The peptides are
XX CC useful as immunological reagents for detecting infection by group O
XX CC human immune deficiency virus (HIV).
XX Sequence 32 AA:
Query Match 84.6%; Score 126; DB 19; Length 32;
Best Local Similarity 85.2%; Pred. No. 4,6e-11;
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETTILNMOORLLNSMCKGKGLVCTYSV 28
DB 1 alettlmqqlinswgcgrlvcysv 27

RESULT 5
ID W07343 standard; peptide: 40 AA.
W07343:
03-JUN-1997 (first entry)
Partial sequence of gp41 from HIV-1 gp. O strain BCF02 (ESS).
DE Human immunodeficiency virus type 1; HIV-1; env; gp. O group O;
XX C2V3-env; gp41; gag; retrovirus; strain; gp. O; variable loop;
XX primer; hybridisation; amplification; Fev; polymerase chain reaction;
XX immunogen; antibody.

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XX OS Human immunodeficiency virus type 1.
XX XX W09627013-AL.
XX PD 06-SEP-1996.
XX PF 26-FEB-1996; 96MO-FR00294.
XX PR 27-FEB-1995; 95FR-0002236.
XX XX (ASST-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX PI Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragostel S, Simon F;
XX WPI: 1996-412779/41.
XX DR N-PSB8; T44918.
XX XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
XX PT antibodies - useful for diagnosis, screening and typing, or as
XX PS immunogens
XX PS Claim 12; Page 33; 71pp; French.
XX CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided
XX CC into 2 major groups based on the nucleotide sequences of the envelope gene
XX CC strains AWT70 and MWP5180. The invention relates to the discovery of
XX CC several new strains of HIV-1 which can be placed in group O, based on the
XX CC partial sequences of the C2V3-env, gp41 and gag genes (see, for example,
XX CC W07329-64). The novel strains have been deposited (BCF02 (MAN), 1547 (BCF08
XX CC I-1544 (BCP02 (ESS)), 1543 (BCF07), 1541 (BCF06) and correspond to a fragment of the gp41 protein
XX CC strain BCF04 (ESS) and corresponds to a fragment of the gp41 protein
XX CC BCF02 (ESS) and the env gene. The nucleic acids can be used to detect gp. O
XX CC HIV-1 strains by hybridisation or (as primers) by gene amplification,
XX CC also for screening and typing of such strains. Peptides encoded by the
XX CC nucleic acids can be used as immunogens to raise Ab for detecting gp. O
XX CC HIV-1.
XX Sequence 40 AA:
Query Match 83.9%; Score 125; DB 17; Length 40;
Best Local Similarity 81.5%; Pred. No. 7,9e-11;
Matches 22; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETTILNMOORLLNSMCKGKGLVCTYSV 28
DB 9 alettlmqqlinswgcgrlvcysv 35

RESULT 6
ID W80472 standard; peptide: 22 AA.
W80472:
28-JAN-1999 (first entry)
Peptide derived from a conserved sequence of group O human HIV.
DE Peptide derived from a conserved sequence of group O human HIV.
XX Group O human immune deficiency virus; HIV; detection; infection.
XX Synthetic.
XX Immune deficiency virus.
XX W09845323-AL.
XX PD 15-OCT-1998.
XX PF 06-APR-1998; 98MO-FR00691.

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XX 24-FEB-1998: 98FR-0002212.
 PR 09-APR-1997: 97FR-0004356.
 XX (SWF) PASTEUR SANOFI DIAGNOSTICS SA.
 XX Chonobaux DMR, Delagrange JFH, Gabelle SXJ, Rieunier FY.
 PI WPI: 1998-583190/49.
 DR
 XX New synthetic peptide(s) - useful for: e.g. detecting infection by
 PT human immune deficiency virus of group O
 PS Claim 6: Page 44: 55pp: French.
 CC M80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent a variable sequence
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 SO Sequence 22 AA:

Query Match 81.9%: Score 122: DB 19: Length 22:
 Best Local Similarity 100.0%: Pred. No. 1,le-10:
 Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 OY 7 LNQORLNSMCKGRKLCVTSY 28
 DB 1 LNqgrLIhswgckgrlvcysv 22

RESULT 7
 M07353
 ID M07353 standard: peptide: 41 AA.
 AC M07353:
 DT 03-JUN-1997 (first entry)
 XX
 XX Partial sequence of gp41 from HIV-1 gp. O strain BCF14.
 XX Human immunodeficiency virus type 1, HIV-1; envelope; group M; group O;
 XX C2V3-env; gp41; gag; retroviral; strain: gp120; hypervariable loop;
 XX primer: hybridisation; amplification; PCR; polymerase chain reaction;
 XX immunogen: antibody.
 KM Human immunodeficiency virus type 1.

PN M09627013-A1.
 XX
 PD 06-SEP-1996.
 XX
 XX 26-FEB-1996: 96MO-FR00294.
 PE
 XX 27-FEB-1995: 95FR-0002236.
 XX
 XX (ASSI-) ASSISTANCE PUBLIQUE HOPITALUX PARIS.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 XX Chaux-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;
 PI WPI: 1996-412779/41.
 XX
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 PT antibodies - useful for diagnosis, screening and typing, or as
 XX immunogens
 XX Claim 12: Page 46: 71pp: French.
 XX Human immunodeficiency virus type 1 (HIV-1) strains are currently divided

CC Into 2 major groups based on the nucleotide sequences of the envelope gene
 CC (env): group M containing sub-groups A-G, and group O containing the
 CC strains AN770 and MY95180. The novel strains of HIV-1 which can be placed on the
 CC several new strains of HIV-1 which can be placed on the discovery of
 CC partial sequences of the C2V3-env, gp41 and gag genes (see T44932 on the
 CC 11/23/94). The novel strains have been deposited as retroviruses CCM08
 CC (NKO) and 1545 (BSP3) (POC). The sequence presented here is from the
 CC strain BCF14 and corresponds to the sequence of the gp41 protein encoded
 CC by the env gene. The nucleotide acids are encoded by the sequence of
 CC strains by hybridisation or (as primers) by gene amplification, also for
 CC screening and typing of such strains. Peptides encoded by the
 CC acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.
 SO Sequence 41 AA:

Query Match 81.2%: Score 121: DB 17: Length 41:
 Best Local Similarity 81.5%: Pred. No. 2, 9e-10:
 Matches 22: Conservative 2: Mismatches 3: Indels 0: Gaps 0:
 OY 2 ALFTLNDQRLNSMCKGRKLCVTSY 28
 DB 9 alftllqndqlhswgckgrlvcysv 35

RESULT 8
 M07350
 ID M07350 standard: peptide: 42 AA.
 AC M07350:
 DT 03-JUN-1997 (first entry)
 XX
 XX Partial sequence of gp41 from HIV-1 gp. O strain BCF09.
 XX Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;
 XX C2V3-env; gp41; gag; retroviral; strain: gp120; hypervariable loop;
 XX primer: hybridisation; amplification; PCR; polymerase chain reaction;
 XX immunogen: antibody.
 XX Human immunodeficiency virus type 1.
 OS
 XX M09627013-A1.
 XX
 PD 06-SEP-1996.
 XX
 XX 26-FEB-1996: 96MO-FR00294.
 PE
 XX 27-FEB-1995: 95FR-0002236.
 XX
 XX (ASSI-) ASSISTANCE PUBLIQUE HOPITALUX PARIS.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 XX Chaux-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;
 PI WPI: 1996-412779/41.
 XX
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 PT antibodies - useful for diagnosis, screening and typing, or as
 XX immunogens
 XX Claim 12: Page 45: 71pp: French.

CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided
 CC into 2 major groups based on the nucleotide sequences of the envelope gene
 CC (env): group M containing sub-groups A-G, and group O containing the
 CC strains AN770 and MY95180. The invention relates to the discovery of
 CC several new strains of HIV-1 which can be placed in group O, based on the
 CC partial sequences of the C2V3-env, gp41 and gag genes (see T44907-39 and
 CC T01329-64). The novel strains have been deposited as retroviruses CCM
 CC (NKO) and 1545 (BSP3) (POC). The sequence presented here is from the

Query match	81.28;	Score 121;	DB 20;	Length 116
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RESULT 11

Query Match	81.28%	Score
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ID Y05625 standard; Protein: 715 AA.
 AC Y05625:
 DE 19-JUL-1999 (first entry)
 DE HIV-1 group O isolate MP645 envelope protein (Env).
 DE HIV-1 group O: Outlier strain; envelope protein; Env; antigen;
 KW vaccine; diagnosis; AIDS.
 KW Human immunodeficiency virus type 1.
 PN M09904011-82.
 PD 28-JAN-1999.
 PF 20-JUL-1998: 98MO-EP04522.
 PR 18-JUL-1997: 97EP-0870110.
 PS (INNO-) INNOGENETICS NV.
 PI Delaporte F, Peeters M, Saman E, Vanden Haesevelde M;
 DR WPI: 1999-132255/11.
 DR N-PDB: X25180.
 PT New isolated HIV-1 group O strains - used to produce
 PT polynucleotide vaccines for use in diagnosis and in
 PT vaccines for prevention of HIV-1 infection
 PS Claim 3: Fig BA: 162pp: English.
 CC The present sequence is a partial Env polypeptide of HIV-1 group O
 CC of MP645 (X25180). The invention relates to new HIV-1 group O
 CC antigens, especially envelope protein antigens (see Y0546-625),
 CC and the use of these antigens for the diagnosis of HIV-1
 CC X25154-80). In the diagnosis and prophylaxis, acids encoding them (see
 CC used as reagents for detecting HIV-1 group O infection and for
 CC differentiating different types of HIV-1 group O infection
 CC Vaccines that provide protective immunity against HIV-1 infection,
 CC one HIV-1 type antigen, a nucleic acid encoding such an antigen,
 CC a virus-like particle, a nucleic acid encoding such an antigen,
 CC form of an HIV-1 type O strain, a polynucleotide vaccine, or an attenuated
 CC HIV-1 group O strains, obtained from patients from Cameroon, Gabon,
 CC Tchad, Nigeria, Senegal and Niger.
 SO Sequence 715 AA:
 SQ
 Query Match Best Local Similarity 81.2%; Score 121; DB 20; Length 715;
 Beat Local Similarity 81.5%; Pred. No. 3.4e-09;
 Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 ALETLINQORLNSWCKGRGLVCTSV 28
 DB 618 aletlqngqlnlwgcgrglvctsv 644
 RESULT 12
 M80470 ID M80470 standard; peptide: 32 AA.
 AC M80470:
 DE 28-JAN-1999 (first entry)
 DE Peptide derived from a conserved sequence of group O human HIV.
 KW Peptide derived from a conserved sequence of group O human HIV.
 KW Group O human immune deficiency virus; HIV; detection; infection.

XX XX Synthetic.
 OS OS Immune deficiency virus.
 OS OS M09845323-A1.
 XX XX 15-OCT-1998.
 PD PD 06-APR-1998: 98MO-FR00691.
 PF PF 24-FEB-1998: 98FR-0002212.
 PR PR 09-APR-1997: 97FR-0004356.
 PS (SNFT) PASTEUR SANOFI DIAGNOSTICS SA.
 PI Chenebaux DMB, Delagrange JFH, Godelle SJX, Rieunier FY;
 DR WPI: 1998-583190/49.
 DR New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 PS Claim 6: Page 44; 55pp: French.
 CC M80459-74 represent synthetic peptides (either linear or cyclized by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC used as reagents for detecting HIV-1 group O infection and for
 CC human immune deficiency virus (HIV).
 SO Sequence 32 AA:
 SQ
 Query Match Best Local Similarity 80.5%; Score 120; DB 19; Length 32;
 Beat Local Similarity 81.5%; Pred. No. 3.1e-10;
 Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 ALETLINQORLNSWCKGRGLVCTSV 28
 DB 1 aletlqngqlnlwgcgrglvctsv 27
 RESULT 13
 M07351 ID M07351 standard; peptide: 41 AA.
 AC M07351:
 DE 03-JUN-1997 (first entry)
 DE Partial sequence of gp41 from HIV-1 gp. O strain BCF12.
 DE Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;
 KW C23Y-env; gp41; gag; retrovirus; amplification; PCR; polymerase chain reaction;
 KW Immunogen; antibody.
 KW Human immunodeficiency virus type 1.
 PN M09627013-A1.
 PD 06-SEP-1996.
 PF 26-FEB-1996: 96MO-FR00294.
 PR 27-FEB-1995: 95FR-0002236.
 PS (ASST-) ASSISTANCE PUBLIQUE HOPITALON PARIS.
 PI (INRM) INSERM INST NAT SANTE & MECH MEDICALE.
 PI Chailly-Baudier M., Loussert-Mjaka I., Ly T., Saragosti S., Simon F.

DR WEI: 1996-412779/1.

XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and
PT protein sequences useful for diagnosis, screening and typing, or as
PT immunogens

XX Claim 12; Page 46; 71pp; French.

CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided
XX into two major groups based on the nucleotide sequences of the envelope gene
CC (env); group M containing sub-groups A-G, and group O containing the
XX strains AN70 and MP5180. The invention relates to the discovery of
CC several new strains of HIV-1 which can be placed in group O. These
XX partial sequences overlap strains have been deposited as retroviruses CIRM
CC I-1544 (BCP02 (GSS)), 1543 (BCP01 (FAN)), 1546 (BCP07 (NAN)), 1547 (BCP08
XX T-1544 (BCP02 (GSS))), 1543 (BCP01 (FAN)). The sequence presented here is from
CC (NKO)) and 1545 (BCP03 (POC)). The sequence presented here is from the
XX strain BCP1 and corresponds to a fragment of the gp4 protein, env, encoded
CC by the env gene. Said the nucleic acid encoders the HIV-1 genome, also for
XX screening and typing of such strains. Peptides encoded by the nucleic
CC acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.
SO Sequence 41 AA;

Query Match	80.5%	Score 120	DB 17	Length 41
Best Local Similarity	77.8%	Prod. NO. 4E-10		
Matches 21	Conservative 3	Mismatches 3	Indels 0	Gaps 0

QY	2	A	L	E	T	L	N	O	R	L	I	N	S	C	K	G	R	I	N	T	S	Y	28
	:		:		:		:		:		:		:		:		:		:		:		
Db	9	a	e	c	t	i	l	i	q	q	i	n	i	w	g	c	y	r	i	t	s	v	35

RESULT	14
ID	Y05559 standard; Protein; 113 AA.
XX	Y05559
AC	Y05559;
DT	19-JUL-1999 (first entry)
DE	HIV-1 group O isolate BSOJ189 gp41 antigen.
XX	HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;
KW	vaccine; diagnosis; AIDS.
XX	Human immunodeficiency virus type 1.
PX	MO9904011-A2.
PD	28-JAN-1999.
PF	20-JUL-1998; 98MO-EF04522.
PR	18-JUL-1997; 97EP-0870110.
PA	(INNO-) INNOGENETICS NV.
P1	Delaporte E, Beeckens M, Saman E, Vanden Heesvelde M;
XX	WPI: 1999-132255/11.
DR	N-PsDB; X25167.
PT	New isolated HIV-1 group O strains - used to produce
PT	polyclonals, anti-gp41 antigens and antibodies for use in diagnosis and in
PT	vaccines for prevention of HIV-1 infection
XX	Claim 3; Fig 6; 16zp; English.
XX	The present sequence is an antigen of the gp41 protein of HIV-1
CC	group O (outlier) strain BSOJ189, a Cameroon isolate. The

[illegible]

Query Match	80.5%	Score 120:	DB 20:	Length 113:
Best Local Similarity	77.8%	Pred. No. 1.1e-09:		
Matches 21:	Conservative 3:	Mismatches 3:	Indels 0:	Gaps 0:
Oy	2	ALETLINQDRLINSGCGEGLCTGYS 28		
		IIIIIIIIIIIIIIIIIIIIIIII		
Db	29	aletlmqgllllwtgckgclcytstv 55		
RESULT 15				
ID	Y05557	standard; Protein, 115 AA.		
XX	Y05557:			
DT	19-JUL-1999	(first entry)		

DE	HIV-1 group O isolate KST008-PW62 gp41 antigen.
XX	
XX	HIV-1 group O: Outlier strain: gp41: envelope protein: antigen:
KW	vaccine: diagnosis: AIDS.
XX	
OS	Human immunodeficiency virus type 1.
XX	MO9904011-42.
XX	
PD	28-JAN-1999.
XX	
PE	20-JUL-1998: 98MO-EP04522.
XX	
PR	18-JUL-1997: 97EP-0870110.
XX	
PA	(INNO-) INNOGENETICS NV.
XX	
PI	Delaporte E, Peeters M, Samaan E, Vanden Haesevelde M;
DR	WPI: 1999-132255/11.
XX	N-PSDB: X25165.
PT	
PJ	New isolated HIV-1 group O strains - used to produce
XX	polyucleotides, antigens and antibodies for use in diagnosis and in
XX	vaccines for prevention of HIV-1 infection
XX	
XX	Claim 3: Fig 6: 16zpp: English.
XX	
CC	The present sequence is an antigen of the gp41 protein of HIV-1
CC	group O (Outlier) strain KST008-PW62, a Nigerian isolate. The
CC	invention relates to new HIV-1 group O antigens (see claim 1) (see
CC	and use of these antigens, or nucleic acids of AIDS. They can be
CC	X25154-40), in the diagnosing HIV-1 group O infection and for
CC	use as assaying different types of HIV-1 group O infection.
CC	Vaccines that provide protective immunity against HIV-1 infection.
CC	particular against HIV-1 group O infection, comprise at least one
CC	HIV-1 type O antigen, a nucleic acid encoding such an antigen, a
CC	virus-like particle comprising such an antigen, or an attenuated
CC	form of an HIV-1 type O strain. The invention also relates to new

CC HIV-1 group O strains, mostly from patients from Cameroon and its
 CC neighbouring countries.
 XX
 SQ Sequence 115 AA:

Query Match 80.58; Score 120; DB 20; Length 115;
 Best Local Similarity 77.88; Pred. No. 1.2e-09;
 Matches 21; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 ALEFLINQORLINSWCKGCRGVCTSV 28
 ||||| : ||||| ||||| : |||||
 DB 29 alelllsgqlnlwgcgkgrllcylsv 55

Search completed: March 22, 2001, 09:51:54
 Job time: 72 sec

No.	Score	Match	Length	Time
1	105	86.1	216	12
2	103	86.1	219	12
3	103	84.4	219	12
4	102	83.6	130	12
5	101	82.8	244	12
6	99	81.1	116	12
7	99	81.1	116	12
8	99	81.1	120	12
9	99	81.1	131	12
10	99	81.1	131	12
11	99	81.1	137	12
12	99	81.1	146	12
13	99	81.1	213	12
14	99	81.1	216	12
15	99	81.1	216	12
16	99	81.1	342	12
17	99	81.1	532	12
18	99	81.1	544	12
19	99	81.1	548	12

20	99	81.1	871	12	057073	057073	human	human
21	99	81.1	872	12	057074	057074	human	human
22	99	81.1	872	12	057072	057072	human	human
23	99	81.1	900	12	090288	090288	human	human
24	98	80.3	114	12	040448	040448	human	human
25	98	80.3	116	12	040445	040445	human	human
26	98	80.3	116	12	040456	040456	human	human
27	98	80.3	119	12	090652	090652	human	human
28	98	80.3	124	12	091387	091387	human	human
29	98	80.3	124	12	091387	091387	human	human
30	99	80.3	134	12	091384	091384	human	human
31	99	80.3	172	12	091383	091383	human	human
32	98	80.3	183	12	091388	091388	human	human
33	98	80.3	200	12	091388	091388	human	human
34	98	80.3	210	12	091388	091388	human	human
35	98	80.3	210	12	091388	091388	human	human
36	98	80.3	212	12	091388	091388	human	human
37	98	80.3	234	12	091388	091388	human	human
38	98	80.3	512	12	091388	091388	human	human
39	98	80.3	512	12	091388	091388	human	human
40	98	80.3	512	12	091388	091388	human	human
41	98	80.3	537	12	091388	091388	human	human
42	98	80.3	547	12	091388	091388	human	human
43	98	80.3	547	12	091388	091388	human	human
44	97	79.5	11	12	040452	040452	human	human
45	97	79.5	11	12	040456	040456	human	human

ALIGNMENTS

RESULT	1	
Q91EC5		
Q91EC5	PRELIMINARY:	PT: 216 AA.
Q91EC5		
Dc	01-OCT-2000 (TREMBL:rel. 15, Created)	
Dc	01-OCT-2000 (TREMBL:rel. 15, Last sequence update)	
Dt	01-OCT-2000 (TREMBL:rel. 15, Last annotation update)	
DE	CP41 (FRAGMENT).	
GN	ENV.	
OS	Human immunodeficiency virus type 1.	
OC	Human immunodeficiency viruses; Retroviridae; Lentivirus.	
OC	NC_017603:Id=11676;	
OR	111	
RN	SEQUENCE FROM N.A.	
RC	STRAIN-BGCF07:	
RA	Rouques P., Robertson D., Sandrine S., Christel D., Francois S.,	
RA	Philippe M.: analysis and subtyping of 47 HIV-1 group O isolates *	
RA	Submitted (JAN-1999) to the EMBL/Genbank/DBD databases.	
DR	EMBL: AJ363394; CMB6543.1; -	
DR	NC_017603:Id=11676	
FT	NOI_TER 1 - 1	
FT	NOI_TER 216 - 216	
QO	SEQUENCE 216 AA; 25027 MW; 413AE9B8B1AEFC9A CRC64;	

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Query Match Similarity      86.1%      Score 105, DB 12; Length 216;
Best Local Similarity      81.8%      Pred. No. 3,9e-09;
Matches      18; Conservative      2; Mismatches      2; Indels      0; Caps      0;

Oy      1 LAMQRLNLSMGCKGRLYCTSV      22
Db      42 IOMQQLNLSMGCKGRLYCTSV      63

RESULT      2
O9IBB6
AC      O9IBB6      PRELIMINARY;      PRT;      219 AA.
DT      01-OCT-2000 (TREMBLeref. 15, Created)
DT      01-OCT-2000 (TREMBLeref. 15, Last sequence update)
DT      01-OCT-2000 (TREMBLeref. 15, Last annotation update)
DE      GP41 (FRAGMENT).

```

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ENV.
OS Human immunodeficiency virus type 1
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN 11
RC SEQUENCE FROM N.A.
RA Philipe M.; Robertson D., Sandrine S., Christel D., Francois S.,
RC STRAIN=SCF1;
RA Philipe M.; Robertson D., Sandrine S., Christel D., Francois S.,
RT *Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.*;
DR Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
EN EMBL: AJ236404; CAB6252.1; -
FT NON_TER 1
FT TER 1
SQ SEQUENCE 219 AA; 25353 MW; F58295EB01520D91 CRC64;

Query Match
Best Local Similarity 86.1%; Score 105; DB 12; Length 219;
Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 1 LNOOILLNSMCKKRLVCYTSV 22
: |||||
DB 52 IONOILLNSMCKKRLVCYTSV 73

RESULT 3
ID Q9IEB3 PRELIMINARY; PRT: 219 AA.
AC Q9IEB3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN 11
RC SEQUENCE FROM N.A.
RA Philipe M.; Robertson D., Sandrine S., Christel D., Francois S.,
RC STRAIN=SCF02;
RA Philipe M.; Robertson D., Sandrine S., Christel D., Francois S.,
RT *Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.*;
DR Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
EN EMBL: AJ236391; CAB6250.1; -
FT NON_TER 1
FT TER 1
SQ SEQUENCE 219 AA; 25363 MW; 85C2DC5B5F528907 CRC64;

Query Match
Best Local Similarity 84.4%; Score 103; DB 12; Length 219;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 1 LNOOILLNSMCKKRLVCYTSV 22
: |||||
DB 51 IONOILLNSMCKKRLVCYTSV 72

RESULT 4
ID Q9IHU9 PRELIMINARY; PRT: 130 AA.
AC Q9IHU9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN 11

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RP SEQUENCE FROM N.A.
RC STRAIN=97CM798;
RA Yang C., Gao F., Fontjuno P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lai F.B.;
RT *Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O.*;
DR EMBL: Y09755; AAF7912.1; -
FT NON_TER 130
FT TER 130
SQ SEQUENCE 130 AA; 15593 MW; 538578A363644EA CRC64;

Query Match
Best Local Similarity 83.6%; Score 102; DB 12; Length 130;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 1 LNOOILLNSMCKKRLVCYTSV 22
: |||||
DB 35 IONOILLNSMCKKRLVCYTSV 56

RESULT 5
ID Q9IEB3 PRELIMINARY; PRT: 242 AA.
AC Q9IEB3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN 11
RC SEQUENCE FROM N.A.
RA Philipe M.; Robertson D., Sandrine S., Christel D., Francois S.,
RC STRAIN=SCF12;
RA Philipe M.; Robertson D., Sandrine S., Christel D., Francois S.,
RT *Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.*;
DR Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
EN EMBL: AJ243366; CAB6336.1; -
FT NON_TER 1
FT TER 1
SQ SEQUENCE 242 AA; 27539 MW; DE8A73DE086AFD7 CRC64;

Query Match
Best Local Similarity 82.8%; Score 101; DB 12; Length 242;
Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

DB 1 LNOOILLNSMCKKRLVCYTSV 22
: |||||
DB 59 IONOILLNSMCKKRLVCYTSV 80

RESULT 6
ID Q0439 PRELIMINARY; PRT: 116 AA.
AC Q0439;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN 11
RC SEQUENCE FROM N.A.
RA Philipe M.; Robertson D., Sandrine S., Christel D., Francois S.,
RC STRAIN=GROUP O;
RA Philipe M.; Robertson D., Sandrine S., Christel D., Francois S.,
RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
EN EMBL: Y09755; CAA70914.1; -

```


DR	INTERPRO: IPR000328; -	
DR	PFAM: PF00517; GP41; 1.	
KW	Transmembrane_1	
FT	NON_TER	1
FT	NON_TER	116
SO	SEQUENCE	116 AA; 13975 MW; 12B3D0DD0D2A1AD32 CRC64.

Query Match	81.1%;	Score 99;	DB 12;	Length 116;
Best Local Similarity	77.3%;	Pred. No. 2e-08;		
Matches 17; Conservative		2; Mismatches 3;	Indels 0;	Caps 0;

```
QY      1 LNQRLNSWGCKGRVCTSV 22
          : | : | | | | | | | | | |
Db      34 IQNQQLNLWGCKGRVCTSV 55
```

RESULT 7
Q40451
Q40451 PRELIMINARY; PRT; 118 AA

01-JAN-1998 (TREMBLrel. 05, Created)
07-01-JAN-1998 (TREMBLrel. 05, last sequence update)
01-MAY-2000 (TREMBLrel. 13, last annotation update)
ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).
DE
03 Human immunodeficiency virus type 1.
VIRUSES: Retroid Viruses; Retroviridae; Lentivirus
OK NCBI Taxid=11676;

Query Match	81.18:	Score 99:	DB 12:	length 118:
Best Local Similarity	77.38:	Prod. No. 28-08:		
Matches 17, Conservative	2;	Mismatches 3;	Indels 0;	Gaps 0:
Qy	1	LNQDRLINSQCKGKGLVCTSY	22	
	:	:-:		
b	34	IQNDQLLMDGCKGKGLVCTSY	55	

RESULT	8	
091HU2		
ID	091HU2	PRELIMINARY; PRT: 120 AA.
AC	091HU2	
DT	01-OCT-2000 (TRIMBLER, 15, Created)	
D7	01-OCT-2000 (TRIMBLER, 15, Last sequence update)	
D7	01-OCT-2000 (TRIMBLER, 15, Last annotation update)	
DE	ENVELOPE GLYCOPROTEIN (FRAGMENT).	
GN	GP41.	
OS	Human immunodeficiency virus type 1.	
OC	viruses; Retrofod viruses; Retroviridae; Lentivirus.	
OX	NCBI_TaxID=11676;	
RN	(1)	
RP	SEQUENCE FROM N.A.	
RC	YKIAAC_97KE205	
RA	YKIAAC_97KE205, Fontjuno P.N., Zekeng L., van der Groen G., Platenjae D., Schable C., Lal R.B.;	
RT	"Phylogenetic analysis of protease and transmembrane regions of HIV type 1 group O.";	
RL	AIDS Res. Hum. Retroviruses 16:1075-1081(2000).	
DR	EMBL; AF23242; AAF1519.1; -	
FT	NON_TER 1	

FT	NON_TERM	120	120
SQ	SEQUENCE	120 AA:	14322 MW: 51DD30863AC87929 CRC64:
Query Match			
Beet Local Similarity	81.1%	Score 99;	DB 12;
Matches 1/; Conservative	77.3%;	Pred. No. 2e-08;	Length 120;
	2;	Mismatches	3;
		Indels	0;
		Gaps	0;

```
QY      1 LNQRLNSWGCKGRVCTSV 22
        : | : | | | | | | | | | |
Db      28 IONOQLNLWGCKGRVCTSV 49
```

RESULT	9
Q9WR05	
ID	Q9WR05
PRELIMINARY;	
PRT;	131 AA

OC Human immunodeficiency virus type 1,
 OX HIV-1; Retrofod viruses; Retroviridae; Lentivirus
 NCBI_TaxId=11676;
 DT 01-NOV-1999 (TREMBLrel_12, Created)
 DT 01-NOV-1999 (TREMBLrel_12, last sequence update)
 DT 01-MAY-2000 (TREMBLrel_13, last annotation update)
 DE ENVELOPE GLYCOPROTEIN [FRAGMENT].
 CN ENV.
 GN

	Query Match	81.1k:	Score 99:	DB 12:	Length 131:
	Best Local Similarity	77.3k:	Pred. No. 2,2e+08:		
	Matches 17:	Conservative	2:	Mismatches 3:	Indels 0:
					Gaps 0:
Qy	1 LNDGRLNSGCKGKGLCYCTSY 22				
	:				
Db	35 IONDGLNLMDGCKGKGLCYCTSY 56				

091HU0	10		
ID	091HU0	PRELIMINARY	PRF: 131 AA.
DC	01-OCT-2000 (TREMblrel. 15, Created)		
DT	01-OCT-2000 (TREMblrel. 15, last sentence update)		
DT	01-OCT-2000 (TREMblrel. 15, last annotation update)		
DE	ENVELOPE GLYCOPROTEIN (FRAGMENT).		
GN	GP41.		
OS	Human immunodeficiency virus type 1.		
OC	Nucleoside triphosphatidyl transferases; Retroviridae; Lentivirus.		
NC	NCLSID=1576;		
PN	111		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-97S202;		
RA	Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,		
RA	Plantasek D., Schibler C.		
FT	Physiogenom O.;		
FT	Physiogenom O.;		
RL	AIDS Res. Hum. Retroviruses 16:1075-1081(2000).		
DR	EMBL: AF229244; AAF11921.1; ..		
FT	NON_TER 1 131		

NON_TIER	146	146
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Query Match	81.1%	Score 99	DB 12	Length 214
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NON_TIER	146	146
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Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNOORLINSWCKGRGLVCTSY 22
 : : ||| ||||| |||||
 Db 40 MONDOLLINWCKGRGLVCTSY 61

RESULT 15

ID O9IEA5 PRELIMINARY; PRT: 216 AA.

AC O9IEA5; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)

DB GPA1 (FRAGMENT).

DE ENA. Ensembl immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

SEQUENCE FROM N.A.

RC STRAIN=VBF26;

RA Roques P., Robertson D., Sandline S., Christel D., Francois S.,

Philippe M., *Phylogenetic analysis and sub-typing of 47 HIV-1 group O Isolates.*

RI Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.

DR EMBU: AJ236415; CAB96263.1;

FT NON_TER 1 1

FT NON_TER 1 1

SO SEQUENCE 216 AA; 25003 MW; 0A5AC218FA88932 CRC64;

Query Match 81.1%; Score 99; DB 12; Length 216;

Best Local Similarity 77.3%; Pred. No. 3.5e-08;

Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNOORLINSWCKGRGLVCTSY 22
 : : ||| ||||| |||||
 Db 37 IONQOLLINWCKGRGLVCTSY 58

Search completed: March 22, 2001, 10:00:47
 Job time: 526 sec

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